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(54) Title: MATERIALS AND METHODS FOR THE MODIFICATION OF ISOPRENOID CONTENT, COMPOSITION AND METABOLISM

(57) Abstract

Novel isolated polynucleotides associated with plant isoprenoid biosynthetic pathways are provided, together with genetic constructs comprising such sequences. Methods for the modulation of the content, structure and metabolism of polypeptides involved in an isoprenoid biosynthetic pathway in target organisms are also disclosed, the methods comprising incorporating one or more of the polynucleotides or genetic constructs of the present invention into the genome of a target organism. Modulation of the content, structure and metabolism of such polypeptides produces modifications in the content, structure and metabolism of isoprenoids in the target organism.

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MATERIALS AND METHODS FOR THE MODIFICATION OF ISOPRENOID CONTENT, COMPOSITION AND METABOLISM

Technical Field of the Invention

This invention relates materials and methods for modifying the content, composition and metabolism of isoprenoids in plants and other organisms. More particularly, this invention relates to polypeptides involved in the synthesis of isoprenoid compounds, such as terpenoid and steroid compounds, polynucleotides encoding such polypeptides, expression of such polypeptides, and methods for modulating the composition and/or expression levels of such polypeptides, thereby modulating isoprenoid content, composition, and metabolism.

Background of the Invention

Isoprenoids form a large family of naturally occurring compounds, with over 20,000 distinct compounds having been described. The isoprenoids include vitamins A, D, E, and K, first recognized as fatty materials essential to the normal growth of animals, and numerous biological pigments. In plants, isoprenoid compounds, including terpenoid and steroid compounds, include hormones such as gibberellic acid and abscisic acid, pigments, electron carriers, membrane components (phytosterols), phytotoxins, antibiotics, flavors such as menthol, vitamins, macromolecular compounds such as rubber and guttapercha, and others.

Isoprene compounds, or prenyl lipids, are composed of one or more basic isoprene skeleton(s) (C_5) formed by the decarboxylation of mevalonate-5-pyrophosphate. From the isopentenyl pyrophosphate ("active isoprene" or "IPP") and the isomeric dimethylallyl pyrophosphate, the geranyl pyrophosphate (C_{10}) may be formed by "head-tail" condensation. By linkage of a further C_5 unit, farnesyl pyrophosphate (C_{15}) is formed. Further extension by "head-tail" or "tail-tail" condensation leads to C_{20}, C_{30} and C_{40} compounds, as well as the higher molecular terpenoids. A schematic diagram of the basic biosynthetic pathways of isoprene compounds is shown in Fig. 1.

IPP is the branching point for a large variety of biologically significant molecules, including isoprenoids, carotenoids, and various sterols in different eukaryotic organisms

(mycosterols, phytosterols and zoosterols). In animals, cholesterols are precursors for several hormones and bile acids. Fungal ergosterol and mammalian cholesterol arise from IPP via squalene oxide and lanosterol, while higher plant sterols, like campesterol and sitosterol, are produced by cyclization of squalene oxide to cycloartenol and by further plant-specific enzymes.

Plant cells contain an intriguing diversity of a subclass of isoprenoids called terpenoids, most of which are cyclic with one or more rings. Terpenes in plants are divided into several classes, including sesquiterpenes, mono-, di-, triterpenes, etc. (Bohlmann *et al.*, *Proc. Natl. Acad. Sci. USA* 95:4126-4133, 1998). Terpenoids are formed by linking isoprene units (C_5H_8) synthesized from acetate. Terpenoids include isoprene (C_5H_8) compounds, including isopen-tenylpyroposphate and active isoprene; monoterpene ($C_{10}H_{16}$) compounds, including geraniol, and from which menthol, camphor, pinene and citronellal are derived; sesquiterpene ($C_{15}H_{24}$) compounds, including farnesol, from which zingiberene, ubiquinone, plastoquinone, abscisic acid and rishitine are derived; diterpene ($C_{20}H_{32}$) compounds, such as geranylgeraniol, from which phytol, kaurene, giberrerellic acid and fusicoccin are derived; triterpene ($C_{30}H_{48}$) compounds, including squalene, from which steriods and saponins are derived; tetraterpene ($C_{40}H_{64}$) compounds, including phytoene and carotenes; and polyterpene $(C_5H_8)_n$ compounds, including rubber and guttapercha.

Synthase enzymes producing terpenes are thought to be of common evolutionary origin, lacking close similarity to other enzymes (except prenyltransferases). Most synthase enzymes have the ability to produce a variety of end-products from a single substrate. This may explain, in part, the enormous diversity of terpenoid compounds found in plants (Mitchell-Olds *et al.*, *Trends in Plant Science* 3(9):362-365, 1998). Complex terpene mixtures are thought to be important plant defensive compounds, their diversity and synergistic action delaying development of resistance in herbivores and pathogens (Langenheim J, *J. Chem. Ecol.* 20:1223-1280, 1994).

Plant terpenoids also have many known medicinal effects, and some plant isoprenoid compounds are administered as drugs. Taxol, which has proven to be efficacious in treating cancer, for example, is derived from terpenoid compounds. Dietary isoprenoids have been suggested to suppress mevalonate pathway, thereby affecting cancer and cardiovascular disease (Elson CE, *J. Nutr.* 125(6 Suppl):1666S-1672S, 1995). Farnesol, the last precursor common to all branches of the mevalonate pathway, has been

demonstrated to inhibit calcium channels in muscle cells (Roullette J-B, *J. Biol. Chem.* 51:32240-32246, 1997).

Ubiquinone and plastoquinone, which are also isoprenoid derivatives, function as electron carriers in the production of ATP in mitocondria and chloroplasts. In most mammalian tissues, ubiquinone (also called coenzyme Q) has ten isoprene units. Plastoquinone is the plant equivalent of ubiquinone. In their role as electron carriers, both ubiquinone and plastoquinone can accept either one or two electrons and either one or two protons to be reduced.

A remarkable role for isoprenyl intermediates has recently been discovered in studies of a protein that is implicated in human cancers and is known to associate with membranes through a covalently bound isoprenyl lipid. This protein, the RAS PROTEIN, is the product of the gene, a mutant version of a normal protein and a number of related GTP-binding proteins. The normal protein and the number of related GTP-binding proteins are known to art in signal transductions triggered by neurotransmitters, hormones, growth factors and other extracellular signals.

Quantitative and qualitative modifications in plant terpenoid content are known to be induced by external factors such as herbivore attack and wounding (Bohlmann J *et al.*, *Proc. Natl. Acad. Sci. USA* 95:6756-6761, 1998). Synthesis of cell terpenoids can also be induced by infection with pathogens. Even agricultural pest insects can be repelled by pine oil terpene compounds: monoterpenes carene, limonene and cymene deter onion flies (Ntiamoah Ya, *Entom. Exp. et Appl.* 79:219-226, 1996).

While the chemical diversity of isoprenoids is well known, and many of the metabolic pathways have been tentatively identified, few of the genes encoding enzymes responsible for the synthesis of isoprenoid compounds have been identified. The present invention is therefore directed to providing novel polynucleotides encoding polypeptides involved in the biosynthesis of isoprenoids, and providing methods for modifying the expression and composition of such polypeptides, thereby modulating isoprenoid content, composition, and metabolism.

Sequencing of the genomes, or portions of the genomes, of numerous biological materials, including humans, animals, microorganisms and various plant varieties, has been and is being carried out on a large scale. Polynucleotides identified using sequencing techniques may be partial or full-length genes, and may contain open reading frames, or portions of open reading frames, that encode polypeptides. Putative polypeptides may be

determined based on polynucleotide sequences. The sequencing data relating to polynucleotides thus represents valuable and useful information.

Polynucleotides may be analyzed for novelty by comparing identified sequences to sequences published in various public domain databases, such as EMBL. Newly identified polynucleotides and putative polypeptides may also be compared to polynucleotides and polypeptides contained in databases to ascertain homology to known polynucleotides and polypeptides. In this way, the degree of similarity or identity or homology of polynucleotides and polypeptides having an unknown function may be determined relative to polynucleotides and polypeptides having known functions.

U.S. Patent 5,589,619 discloses materials and methods for increasing squalene and sterol accumulation in higher plants by modifying the copy number of a gene encoding a polypeptide having HMG-CoA reductase activity. Genetic materials, including polynucleo-tides, polypeptides, DNA molecules, and the like, relating to HMG-CoA reductase activity are disclosed, as well as methods for transforming plant cells and producing transgenic plants.

U.S. Patent 5,689,047 discloses stilbene synthase genes derived from grapevines, as well as the use of those genes in vectors and transformed microorganisms, as well as transformed plant cells and plants.

U.S. Patent 5,753,507 discloses plant polynucleotides encoding geraniol/nerol 10 – hydroxylase ($G_{10}H$), as well as methods for using complete and partial polynucleotides as probes, and methods for expressing $G_{10}H$ and enhancing levels of terpenoid indole alkaloid and ividoid insect pheromone produced by a plant.

The following U.S. Patents disclose isoprenoid compounds or related compounds, or methods for using such compounds: U.S. Patent 5,429,939; U.S. Patent 5,444,166; U.S. Patent 5,460,949; U.S. Patent 5,470,832; U.S. Patent 5,474,925; U.S. Patent 5,495,070; U.S. Patent5,521,078; U.S. Patent 5,545,816; U.S. Patent 5,547,856; U.S. Patent 5,569,832; U.S. Patent 5,580,963; U.S. Patent 5,597,718; U.S. Patent 5,670,349; U.S. Patent 5,674,485; U.S. Patent 5,684,238; U.S. Patent 5,689,056; U.S. Patent 5,691,147; U.S. Patent 5,693,476; and U.S. Patent 5,443,978. The U.S. Patents cited above are incorporated by reference herein in their entireties.

Summary of the Invention

Briefly, the present invention provides isolated polynucleotides encoding polypeptides involved in the production and modification of isoprenoids. Genetic constructs comprising such sequences and methods for the use of such genetic constructs are also provided, together with transgenic cells and plants incorporating such genetic constructs and exhibiting modified isoprenoid content, composition, and metabolism.

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-53 and 78-164, variants of those sequences, extended sequences comprising the sequences set out in SEQ ID NOS: 1-53, 78-164 and their variants, probes and primers corresponding to the sequences set out in SEQ ID NOS: 1-53, 78-164 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164 (*x*-mers), and extended sequences comprising portions of the sequences set out in SEQ ID NOS: 1-53 and 78-164, all of which are referred to herein, collectively, as "polynucleotides of the present invention."

The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NOS: 165-304, polypeptide variants of those sequences, polypeptides comprising the isolated polypeptide sequences and variants of those sequences, polypeptides comprising at least a specified number of contiguous residues of any of the polypeptides identified as SEQ ID NOS: 165-304; and polypeptides comprising portions of the sequences set out in SEQ ID NOS: 165-304.

The polynucleotide sequences identified as SEQ ID NOS: 1-53 and 78-164 were derived from plant sources, namely from *Eucalyptus grandis* and *Pinus radiata*. The polynucleotides of the present invention are primarily "partial" sequences, in that they do not represent a full length gene encoding a full length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. The partial sequences identified as SEQ ID NOS: 1-53 and 78-164 may thus be extended until an open reading frame encoding a polypeptide, a full length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NOS: 1-53 and 78-164 or a variant thereof, or a portion of one of the sequences of SEQ ID NOS: 1-53

and 78-164 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (*x*-mer) of one of the sequences of SEQ ID NOS: 1-53 and 78-164 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-53 and 78-164.

The polynucleotides identified as SEQ ID NOS: 1-53 and 78-164 may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full length sequences corresponding to the sequences set out as SEQ ID NOS: 1-53 and 78-164. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet at http://www.ncbi.nlm.nih.gov/gorf/gorf.html. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, polynucleotides and open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible DNA constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such DNA constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells.

Polypeptides encoded by the polynucleotides of the present invention may be expressed and used in various assays to determine their biological activity. Such polypeptides may be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

The present invention also contemplates methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving, according to one embodiment, stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant, preferably a woody plant, more preferably a woody plant of the *Pinus* or *Eucalyptus* species, and most preferably *Eucalyptus grandis* or *Pinus radiata*. In a related aspect, a method for producing an organism having an altered genotype or phenotype is provided, the method comprising transforming a host cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to growth and regeneration. Organisms having an altered genotype or phenotype as a result of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such organisms and progeny of such organisms, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-53, 78-164, and their variants, may be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be used to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray technologies, including the microarray technology used by Synteni (Palo Alto, CA).

The polynucleotides of the present invention may also be used to tag or identify an organism or reproductive material therefrom. Such tagging may be accomplished, for example, by stably introducing a non-disruptive non-functional heterologous

polynucleotide identifier into an organism, the polynucleotide comprising one of the polynucleotides of the present invention.

The polynucleotides of the present invention encode polypeptides that have activity in an isoprenoid biosynthetic pathway. The isoprenoid metabolism-related polynucleotides were isolated from pine and eucalyptus, and putatively identified by DNA and protein similarity searches. Various isoprenoid compounds are well characterized and have useful properties. Methods of the present invention relating to modulating the polynucleotide and/or polypeptide content and composition of an organism and, thereby, modulating the isoprenoid content, composition and metabolism of an organism, are applicable to a wide range of activities. The novel materials and methods of the present invention have a multitude of potential uses: in forestry and agriculture for manipulation of isoprenoid metabolism; in medicine for therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms; in fermentation and chemical processing industries involving isoprenoids; and in numerous other applications, some of which are described in the references cited above. In plant applications, manipulating isoprenoid pathways or isoprenoid composition may, for example, affect plant development, pest resistance, and the value of extractives (pinene, myrcene, etc.). In foodstuffs, various isoprenoids affect the nutritional quality and pharmacological properties of the ingested material, *e.g*, cholesterol or phytosterol composition of animal-derived and plant-derived foods for human or animal consumption. Additionally, isoprenoid pathways control the production of vitamins A, E, and K; plant pigments such as carotene and the phytol chain of chlorophyll; natural rubber; many essential oils, such as the fragrant principles of lemon oil, eucalyptus, and musk; insect juvenile hormone, which controls metamorphosis; dolichols, which serve as lipid-soluble carriers in complex polysaccharide synthesis; and ubiquinone and plastoquinone, electron carriers in mitochondria and chloroplasts. The ubiquitous and varied roles of isoprenoids thus make these compounds and the polynucleotides encoding them attractive targets for biotechnical applications in a variety of fields.

Briefly, the present invention provides isolated polynucleotides encoding polypeptides involved in the synthesis of isoprenoids. The polynucleotides and polypeptides of the present invention have demonstrated similarity to polypeptides that are known to be involved in the synthesis of isoprenoids as shown below in Table 1.

TABLE 1

POLYNUCLEOTIDE SEQ ID NO	POLYPEPTIDE SEQ. ID	POLYPEPTIDE IDENTITY
1	252	Acetylcholinesterase Precursor
2	253	Deoxyxylulosephosphate Synthase (DXPS)
3, 4, 44	254,255,295	Geranyltranstransferase
5, 6	256,266	Farnesyltranstransferase
7, 154	258 241	Squalene Synthetase
8-10, 155-157	259-261 242-244	Squalene Monooxygenase
11	262	Geranylgeranyl-Diphosphate Geranylgeranyltransferase
12	263	Trichodiene Synthase
13, 25, 84-88, 95 115-118	264,276 171-175, 182, 202-205	Pinene Synthase
14, 89, 90	265 176, 177	Abietadine Synthase
15, 91-94, 96-98, 131-135	266 178-181, 183-185, 218-222	Hydroxymethylglutaryl-Coa Reductase (NADPH)
16, 17, 18, 99-102	267,268,269, 186-189	Myrcene Synthase
19, 20, 103, 107, 108	270,271 190, 194, 195	Limonene Synthase
21-23, 109-111	272-274 196-198	Cadinene Synthase
24, 114	275 201	Bisabolene Synthase
26, 27	277,278	Pinene/Myrcene/Limonene Synthase
28, 119-122	279 206-209	Cycloartenol Synthase
29, 124-126	280 211-213	Obtusifoliol Demethylase
30	281	Lupeol Synthase
31, 158, 159	282 245, 246	Udp-Glucose:Sterol Glucosyltransferase
32	283	Hydroxymethylglutaryl-CoA Reductase (NADPH)
33, 34, 160-162	284,285 247-249	Sterolmethyltransferase
35, 136	286 223	Lecithin:Cholesterol Acyl Transferase
36, 137	287 224	Sterol Delta-7 Reductase
37, 38, 138-140	288,289 225-227	Methyl Sterol Oxidase
39	290	Deoxyxylulosephosphate Synthase (DXPS)
40	291	Phosphomevalonate Kinase
41, 50, 141, 142, 146	292,301 228, 229, 233	Diphosphomevalonate Decarboxylase
42, 43, 143	293,294 230	Isopentenyl-Diphosphate Delta-Isomerase

POLYNUCLEOTIDE SEQ ID NO	POLYPEPTIDE SEQ. ID	POLYPEPTIDE IDENTITY
45	296	Estradiol Dehydrogenase
46-49, 144, 145	297-300 231, 232	Furostanol Glucosidase
51, 52, 147-153	302,303 234-240	Oxysterol-Binding Protein
53	304	Sterol Carrier Protein
78, 79, 127-130	165, 166, 214-217	Sterol 14-demethylase
81	168	Sesquiterpene cyclase
82, 83	169, 170	Geranylgeranyl diphosphate
104-106, 164	191-193, 251	CXPS/transketolase
112, 113	199, 200	Sabinene synthase
123	210	Beta-amyrin synthase
163	250	Sterol desaturase

In one embodiment, the isolated polynucleotides comprise a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 1-53 and 78-164; (b) complements of the sequences recited in SEQ ID NOS: 1-53 and 78-164; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-53 and 78-164; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-53 and 78-164; and (e) sequences having either 40%, 60%, 75% or 90% identity, as defined herein, to a sequence of (a) – (d) or a specified region of a sequence of (a) – (d).

In a further aspect, isolated polypeptides encoded by the polynucleotides of the present invention are provided. In one embodiment, such polypeptides comprise an amino acid sequence encoded by polynucleotides of the present invention, including polynucleotides comprising a sequence set out in the group consisting of SEQ ID NOS: 1-53 and 78-164, as well as polypeptides comprising an amino acid sequence recited in SEQ ID NOS: 165- 304.

In another aspect, the invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, in combination with one or more additional polynucleotides of the present invention, or in combination with one or more known polynucleotides, together with transgenic cells comprising such constructs.

In a related aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of an enzyme encoded by an inventive polynucleotide or a variant thereof; and a gene termination sequence. The open reading frame may be oriented in either a sense or antisense direction. Genetic constructs comprising a non-coding region

of a gene coding for an enzyme encoded by the above polynucleotide or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Genetic constructs comprising, in the 5' – 3' direction, a promoter sequence; a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide comprising a polynucleotide of the present invention; or (2) a polynucleotide comprising a polynucleotide of the present invention and including a non-coding region of a gene coding for a polypeptide having activity in an isoprenoid biosynthetic pathway, are also contemplated. The genetic construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic host cells, such as transgenic plant cells, comprising the genetic constructs of the present invention are provided, together with plants comprising such transgenic cells, and fruits, seeds, and progeny of such plants. Other useful host cells include bacterial cells, insect cells, yeast cells and mammalian cells.

In yet another aspect, methods for modulating the isoprenoid content, composition, and metabolism of an organism are provided, such methods including stably incorporating into the genome of the organism a genetic construct of the present invention. In a preferred embodiment, the target organism is a plant and the plant is a woody plant, preferably selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species, more preferably from the group consisting of pine and eucalyptus species, and most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*. In a related aspect, a method for producing an organism having modified isoprenoid content is provided, the method comprising transforming a host cell with a genetic construct of the present invention to provide a transgenic cell and cultivating the transgenic cell under conditions conducive to growth and regeneration.

In yet a further aspect, the present invention provides methods for modifying the activity of a polypeptide in a target organism such as a plant, comprising stably incorporating into the genome of the organism a genetic construct of the present invention. In a preferred embodiment, the target organism is a plant, and the plant is a woody plant, preferably selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species, more preferably from the group consisting of pine and eucalyptus species, and most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*.

In yet a further aspect, the present invention provides methods for modulating one or more of the content, the composition and the metabolism of an isoprenoid compound in an organism by administering an isolated polypeptide of the present invention to the organism. In applications in which the organism is a plant, administration of the polypeptide may be topical, such as by spraying or similar topical application. In applications in which the organism is mammalian, administration of the polypeptide may be systemic, such as by injection, intradermal delivery, oral delivery, delivery via nasal passageways or airways, or the like.

The above-mentioned and additional features of the present invention and the manner of obtaining them will become apparent, and the invention will be best understood by reference to the following more detailed description.

Description of Drawings

Fig. 1 shows a schematic diagram illustrating basic biosynthetic pathways of isoprene compounds.

Fig. 2 illustrates genomic DNA samples from tobacco plants created in a tagging experiment using a unique sequence identifier from *Pinus* (left panel) and a unique sequence identifier from *Eucalyptus* (right panel). In both panels, Lanes A and B contain DNA samples from empty-vector transformed control plants and Lanes C-E contain DNA samples from plants transformed with a unique sequence identifier.

Fig. 3 illustrates detection of a *Pinus* unique sequence identifier in transformed tobacco plants. Lanes A and B show the hybridization of a probe from SEQ ID NO: 76 to the genomic DNA of tobacco plants which lack the *Pinus* unique sequence identifier (empty-vector transformed control plants). Lanes C-E show the hybridization of the probe to the genomic DNA of tobacco plants containing one to three copies of the *Pinus* unique sequence identifier.

Fig. 4 illustrates detection of a *Eucalyptus* unique sequence identifier in transformed tobacco plants. Lanes A and B show the hybridization of a probe from SEQ ID NO: 77 to the genomic DNA of tobacco plants which lack the *Eucalyptus* unique sequence identifier (empty-vector transformed control plants). Lanes C-E show the hybridization of the probe to the genomic DNA of tobacco plants containing one to two copies of the *Eucalyptus* unique sequence identifier.

Detailed Description

As described above, isoprenoids are important components in a variety of eukaryotic functions. Modification of isoprenoid content, composition, and metabolism in the earlier parts of the pathway, especially the steps up to the formation of isopentenyl-diphosphate (IPP), geranyl-diphosphate (GPP), farnesyl-diphosphate (FPP) and squalene, may have a profound influence on the synthesis of the isoprenoid compounds deriving from these two precursors. Blocking one or more of the downstream steps branching from isopentenyl-diphosphate and squalene may also have a substantial effect on the pool of isopentenyl-diphosphate and squalene available for synthesis of terpenes or steroids. Hence, modifi-cations in the synthesis, content, composition, and metabolism of any single enzyme in the isoprenoid biosynthetic pathway, and particularly in the early part of the pathway (IPP => GPP => FPP => squalene) of the isoprenoid synthesis, may affect the content, composition and metabolism of terpenoid and steroid compounds.

Using the methods and materials of the present invention, the isoprenoid content of a plant may be modified by incorporating sense or antisense copies of polynucleotides encoding polypeptides involved in the synthesis of isoprenoids into the genome of a target organism. In addition, the number of copies and combination of polynucleotides encoding for different enzymes in the biosynthetic pathway of isoprenoids may be manipulated to modify the relative amounts of isoprenoids synthesized, thereby producing biological materials having an altered composition and/or altered isoprenoid metabolism. Similarly, the alteration of isoprenoid composition, for direct application in a target organism, or for production of polypeptides for separate use, is advantageous for a variety of applications, as evidenced by the references cited above and incorporated herein by reference.

According to one embodiment, the present invention provides isolated polynucleotides encoding, or partially encoding, polypeptides having similarity to polypeptides known to be involved in isoprenoid synthesis and modification. The polynucleotides of the present invention were isolated from eucalyptus and pine species, but may alternatively be isolated from other plant sources and may be synthesized using conventional synthesis techniques. Specifically, isolated polynucleotides of the present invention comprise: the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164; complements of the sequences identified as SEQ ID NOS: 1-53 and 78-164; reverse sequences of the sequences identified as SEQ ID NOS: 1-53 and 78-164; reverse complements of the sequences identified as SEQ ID NOS: 1-53 and 78-164; at least a

specified number of contiguous residues (x-mers) of any of the above-mentioned polynucleotides; polynucleotides complementary to any of the above polynucleotides; anti-sense sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification.

The isolated polynucleotides recited in SEQ ID NOS: 1-53 and 78-164 encode, or partially encode, polypeptides demonstrating sequence similarity to polypeptides known to be involved in an isoprenoid biosynthetic pathway, as indicated in Table 1 above. More specifically, the isolated polynucleotides listed in the first column of Table 1 encode, or partially encode the polypeptides listed in alignment in the second column of Table 1, above. Predicted amino acid sequences corresponding to the polynucleotides set out in SEQ ID NOS: 1-53, 78-164, based on information available at the time of filing this application, are provided in SEQ ID NOS: 165-304, as indicated in Table 1.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. A gene is a polypeptide that codes for a functional polypeptide or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki *et al.*, *Artific. Organs* 20(8):836-848, 1996. Polynucleotides of the present invention also encompass polynucleotide sequences that differ from the disclosed sequences but which, as a result of the degeneracy of genetic code, encode a polypeptide which is the same as that encoded by a polynucleotide of the present invention.

The definitions of the terms "complement," "reverse complement," and "reverse sequence," as used herein, are best illustrated by the following examples. For the

sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequences are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'

Identification of genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All of the polynucleotides described herein are isolated and purified, as those terms are commonly used in the art.

In another aspect, the present invention provides isolated polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide which comprises an isolated polypeptide or variant provided herein. In one embodiment, polypeptides of the present invention comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 165-304, as well as variants of such sequences. According to another embodiments, polypeptides of the present invention comprise at least a specified number of contiguous residues (x-mers) of any of the sequences provided in SEQ ID NOS: 165-304.

Polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polypeptide encoding a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *Escherichia coli*, insect, yeast or a mammalian cell line such as COS or CHO. The

polynucleotide(s) expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 165-304, and variants thereof. As used herein, a "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

A functional portion comprising an active site may be made up of separate portions present on one or more polypeptide chains and generally exhibits high substrate specificity. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide comprising a partial isolated polynucleotide of the present invention.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques that are well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2154, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagensis (Kunkel T, *Proc. Natl. Acad. Sci. USA*

82: 488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure form. Preferably, the polypeptides are at least about 80% pure; more preferably at least about 90% pure; and most preferably, at least about 99% pure. In certain preferred embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends polynucleotide or polypeptide sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant polynucleotide sequences preferably exhibit at least 40%; more preferably at least 60%; more preferably yet at least 75%; and most preferably at least 90% identity to a sequence of the present invention. Variant polypeptide sequences preferably exhibit at least 50%; more preferably at least 75%; more preferably yet at least 90%; and most preferably at least 95% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide and polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The percentage identity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTX and BLASTP programs are available on the NCBI anonymous FTP server (ftp://ncbi.nlm.nih.gov) under /blast/executables/. The BLASTN algorithm Version 2.0.4 [Feb-24-1998] and Version 2.0.6 [Sept-16-1998], set to the parameters described below, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, set to the parameters

described below, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP, and BLASTX, is described at NCBI's website at URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html and in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25: 3389-3402, 1997.

The computer algorithm FASTA is available on the Internet at the ftp site ftp://ftp.virginia.edu/pub/fasta/. Version 2.0u4 [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, may be also used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson WR, *Methods in Enzymol.* 183: 63-98, 1990.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotide sequences: Unix running command: blastall -p blastn -d embldb -e 10 –G0 -E0 -r 1 -v 30 -b 30 -i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; and -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 –v 30 –b 30 –i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional. The "hits" to one or more database sequences by a queried sequence produced by BLASTN, FASTA, BLASTP or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN, FASTA, and BLASTP algorithms also produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the polynucleotide sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN, FASTA, or BLASTP algorithms set at parameters described above. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at parameters described above. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as a polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the parameters described above.

Alternatively, variant polynucleotides or polypeptides of the present invention comprise a sequence exhibiting at least 40%; more preferably at least 60%; more preferably yet at least 75%; and most preferably at least 90% identity to a polynucleotide or polypeptide of the present invention, determined as described below. The percentage

identity is determined by aligning sequences using one of the BLASTN, FASTA, or BLASTP algorithms, set at the running parameters described above, and identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. For example, a polynucleotide of the present invention having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the parameters described above. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the polynucleotide of the present invention to the hit in the EMBL library is thus 21/220 times 100, or 9.5%. The polynucleotide sequence in the EMBL database is thus not a variant of a polynucleotide of the present invention.

Alternatively, variant polynucleotides of the present invention hybridize to the polynucleotide sequences recited in SEQ ID NOS: 1-53 and 78-164, or complements, reverse sequences, or reverse complements of those sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65° C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity as a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NOS: 1-53 and 78-164, or complements, reverse sequences, or reverse complements of those sequences as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NOS: 1-53 and 78-164, or complements, reverse complements, or reverse sequences as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NOS: 165-304 as a result of

amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by an encompassed within the present invention, provided the variant polypeptide has activity in an isoprenoid biosynthetic pathway.

The polynucleotides of the present invention may be isolated from various libraries, or may be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Some of the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164 are referred to as "partial" sequences, in that they do not represent the full coding portion of a gene encoding a naturally occurring polypeptide. The partial polynucleotide sequences disclosed herein may be employed to obtain the corresponding full length genes for various species and organisms by, for example, screening DNA expression libraries using hybridization probes based on the polynucleotides of the present invention, or using PCR amplification with primers based upon the polynucleotides of the present invention. In this way one can, using methods well known in the art, extend a polynucleotide of the present invention upstream and downstream of the corresponding mRNA, as well as identify the corresponding genomic DNA, including the promoter and enhancer regions, of the complete gene. The present invention thus comprehends isolated polynucleotides comprising a sequence identified in SEQ ID NOS: 1-53 and 78-164, or a variant of one of the specified sequences, that encode a functional polypeptide, including full length genes. Such extended polynucleotides may have a length of from about 50 to about 4,000 nucleic acids or base pairs, and preferably have a length of less than about 4,000 nucleic acids or base pairs, more preferably yet a length of less than about 3,000 nucleic acids or base

pairs, more preferably yet a length of less than about 2,000 nucleic acids or base pairs. Under some circumstances, extended polynucleotides of the present invention may have a length of less than about 1,800 nucleic acids or base pairs, preferably less than about 1,600 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably yet less than about 1,200 nucleic acids or base pairs, and most preferably less than about 1,000 nucleic acids or base pairs.

Polynucleotides of the present invention also comprehend polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164, complements, reverse sequences, and reverse complements of such sequences, and their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polypeptides identified as SEQ ID NOS: 165-304, and their variants. As used herein, the term "*x*-mer," with reference to a specific value of "*x*," refers to a sequence comprising at least a specified number ("*x*") of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164, or the polypeptides identified as SEQ ID NOS: 165-304. According to preferred embodiments, the value of *x* is preferably at least 20; more preferably, at least 40; more preferably yet, at least 60; and most preferably, at least 80. Thus, polynucleotides and polypeptides of the present invention comprise a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide or polypeptide identified as SEQ ID NOS: 1-53, and 78-304, and variants thereof.

Polynucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-53 and 78-164, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest. As used herein, the term "oligonucleotide" refers to a relatively short segment of a polynucleotide sequence, generally comprising between 6 and 60 nucleotides, and comprehends both probes for use in hybridization assays and primers for use in the amplification of DNA by polymerase chain reaction.

An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-53 and 78-164, or a variant, if the oligonucleotide probe or primer, or its

complement, is contained within one of the sequences set out as SEQ ID NOS: 1-53 and 78-164, or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand selectively hybridizes to a second DNA strand under stringent hybridization conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM and preferably less than about 200 mM. Hybridization temperatures may be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. The DNA from plants or samples or products containing plant material can be either genomic DNA or DNA derived by preparing cDNA from the RNA present in the sample.

In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. In addition, artificial analogs of DNA hybridizing specifically to target sequences could also be used.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably, from about 10 to 50 base pairs in length or, more preferably, from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops and other factors, which are well known in the art. Tools and software

suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example, at URL http://www.horizonpress.com/pcr/. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach CW and Dyksler GS, *PCR primer: a laboratory manual*. CSHL Press: Cold Spring Harbor, NY, 1995.

A plurality of oligonucleotide probes or primers corresponding to a polynucleotide of the present invention may be provided in a kit form. Such kits generally comprise multiple DNA or oligonucleotide probes, each probe being specific for a polynucleotide sequence. Kits of the present invention may comprise one or more probes or primers corresponding to a polynucleotide of the present invention, including a polynucleotide sequence identified in SEQ ID NOS: 1-53 and 78-164.

In one embodiment useful for high-throughput assays, the oligonucleotide probe kits of the present invention comprise multiple probes in an array format, wherein each probe is immobilized in a predefined, spatially addressable location on the surface of a solid substrate. Array formats which may be usefully employed in the present invention are disclosed, for example, in U.S. Patent Nos. 5,412,087 and 5,545,531; and PCT Publication No. WO 95/00530, the disclosures of which are hereby incorporated by reference.

Probes, preferably in the form of an array, may be employed to screen for differences in organisms or samples or products containing genetic material using high throughput screening techniques that are well known in the art. The significance of using probes in high-throughput screening systems is apparent for applications such as plant breeding and quality control operations in which there is a need to identify large numbers of seed lots and plant seedlings, to examine samples or products for unwanted plant materials, to identify plants or samples or products containing plant material for quarantine purposes, etc., or to ascertain the true origin of plants or samples or products containing plant material. Screening for the presence or absence of polynucleotides of the present invention used as identifiers for tagging plants is valuable for later detecting the amount of gene flow in plant breeding, introgression of genes via dispersed pollen, etc.

In this manner, oligonucleotide probe kits of the present invention may be employed to examine the presence/absence (or relative amounts in case of mixtures) of polynucleotides in different samples or products containing different materials rapidly and in a cost-effective manner. Examples of plant species that may be examined using the

present invention, include forestry species, such as pine and eucalyptus species, other tree species, and agricultural and horticultural plants.

Another aspect of the present invention involves collections of a plurality of polynucleotides of the present invention. A collection of a plurality of the polynucleotides of the present invention, particularly the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164, and variants thereof, may be recorded and/or stored on a storage medium and subsequently accessed for purposes of analysis, comparison, etc. Suitable storage media include magnetic media such as magnetic diskettes, magnetic tapes, CD-ROM storage media, optical storage media, and the like. Suitable storage media and methods for recording and storing information, as well as accessing information such as polynucleotide sequences recorded on such media, are well known in the art. The polynucleotide information stored on the storage medium is preferably computer-readable and may be used for analysis and comparison of the polynucleotide information.

According to one embodiment, the storage medium includes a collection of at least 4, preferably at least 10, more preferably at least 15, and most preferably at least 20 of the polynucleotides of the present invention, preferably the polynucleotides identified as SEQ ID NOS: 1-53 and 78-164, and variants of those polynucleotides.

For applications where modulation of a polypeptide involved with isoprenoid biosynthesis and/or isoprenoid metabolism is desired, an open reading frame may be inserted into a genetic construct in a sense or antisense orientation, such that transformation of a target plant with the genetic construct produces a change in the expression level of the polypeptide compared to the expression in a wild-type organism. Transformation with a genetic construct comprising an open reading frame in a sense orientation will generally result in modulation of expression of the selected gene, while transformation with a genetic construct comprising an open reading frame in an antisense orientation generally produces reduced expression of the selected gene. A population of plants transformed with a genetic construct comprising an open reading frame of the present invention in either a sense or antisense orientation may be screened for increased or reduced expression of the gene in question using techniques well known to those of skill in the art, and plants having the desired phenotypes may thus be isolated.

Alternatively, expression of a gene involved in the biosynthesis of isoprenoids may be inhibited by inserting a portion of an open reading frame of the present invention, in either sense or antisense orientation, in the genetic construct. Such portions need not be

full-length but preferably comprise at least 25, and more preferably, at least 50 residues of polynucleotide of the present invention. A much longer portion, or even the full length polynucleotide corresponding to the complete open reading frame, may be employed. The portion of the open reading frame does not need to be precisely the same as the endogenous sequence, provided that there is sufficient sequence similarity to achieve inhibition of the target gene. Thus a sequence derived from one species may be used to inhibit expression of a gene in a different species.

According to another embodiment, the genetic constructs of the present invention comprise a polynucleotide including a non-coding region of a gene coding for a polypeptide encoded by a polynucleotide of the present invention, or a polynucleotide complementary to such a non-coding region. Examples of non-coding regions which may be usefully employed in such constructs include introns and 5'-non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of an isoprenoid compound synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990 and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (e.g. DNA or RNA) in ribozyme constructs (McIntyre CL and Manners JM, *Transgenic Res.* 5(4):257-262, 1996). Ribozymes are synthetic RNA molecules that comprise a hybridizing region complementary to two regions, each of which comprises at least 5 contiguous nucleotides in a mRNA molecule encoded by one of the inventive polynucleotides. Ribozymes possess highly specific endonuclease activity, which autocatalytically cleaves the mRNA.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the polypeptide. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist downstream of the open reading frame or in introns (Luehrsen KR, *Mol. Gen. Genet.* 225:81-93, 1991); or in the coding region, as for example in a plant defence gene (Douglas *et al.*, *EMBO J.* 10:1767-1775, 1991). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For

genetic constructs comprising either an open reading frame in an antisense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

Numerous gene promoter sequences that may be usefully employed in the genetic constructs of the present invention are well known in the art. The gene promoter sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are common to those of the polynucleotide being introduced.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter with or without enhancers, such as the Kozak sequence or the Omega enhancer, and *Agrobacterium tumefaciens* nopalin synthase terminator, may be usefully employed in the present invention. Use of a tissue specific promoter will result in production of the desired sense or antisense RNA only in the tissue of interest. With genetic constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as eucalyptus or pine are used. Other examples of gene promoters which may be usefully employed in the present invention include mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in target cells, such as plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers et al. *in* Weissbach A and Weissbach H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Transformed cells can thus be identified by their ability to grow in media containing the antibiotic in question. Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots. A transcription initiation site may additionally included in the genetic construct when the sequence to be transcribed lacks such a site.

Techniques for operatively linking the components of the genetic constructs of the present invention are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, *Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989. The DNA construct of the present invention may be linked to a vector having at least one replication system, for example *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of target organisms such as plants, both monocotyledonous (*e.g.*, grasses, corn, grains, oat, wheat and barley); dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple); gymnosperms (*e.g.*, Scots pine (Aronen, *Finnish Forest Res. Papers*, Vol. 595, 1996); white spruce (Ellis *et al.*, *Biotechnology* 11: 84-89, 1993); and larch (Huang *et al.*, *In Vitro Cell* 27:201-207, 1991). In a preferred embodiment, the inventive DNA constructs are employed to transform woody plants, herein defined as a tree or shrub whose stem lives for a number of years and increases in diameter each year by the addition of woody tissue. Preferably the target plant is selected from the group consisting of eucalyptus and pine species, most preferably from the group consisting of *Eucalyptus grandis* and *Pinus radiata*. Other species which may be usefully transformed with the DNA constructs of the present invention include, but are not limited to: Pines, such as

Pinus banksiana, Pinus brutia, Pinus caribaea, Pinus clausa, Pinus contorta, Pinus coulteri, Pinus echinata, Pinus eldarica, Pinus ellioti, Pinus jeffreyi, Pinus lambertiana, Pinus monticola, Pinus nigra, Pinus palustrus, Pinus pinaster, Pinus ponderosa, Pinus resinosa, Pinus rigida, Pinus serotina, Pinus strobus, Pinus sylvestris, Pinus taeda, Pinus virginiana; other gymnosperm, such as *Abies amabilis, Abies balsamea, Abies concolor, Abies grandis, Abies lasiocarpa, Abies magnifica, Abies procera, Chamaecyparis lawsoniona, Chamaecyparis nootkatensis, Chamaecyparis thyoides, Huniperus virginiana, Larix decidua, Larix laricina, Larix leptolepis, Larix occidentalis, Larix siberica, Libocedrus decurrens, Picea abies, Picea engelmanni, Picea glauca, Picea mariana, Picea pungens, Picea rubens, Picea sitchensis, Pseudotsuga menziesii, Sequoia gigantea, Sequoia sempervirens, Taxodium distichum, Tsuga canadensis, Tsuga heterophylla, Tsuga mertensiana, Thuja occidentalis, Thuja plicata;* and Eucalypts, such as *Eucalyptus alba, Eucalyptus bancroftii, Eucalyptus botyroides, Eucalyptus bridgesiana, Eucalyptus calophylla, Eucalyptus camaldulensis, Eucalyptus citriodora, Eucalyptus cladocalyx, Eucalyptus coccifera, Eucalyptus curtisii, Eucalyptus dalrympleana, Eucalyptus deglupta, Eucalyptus delagatensis, Eucalyptus diversicolor, Eucalyptus dunnii, Eucalyptus ficifolia, Eucalyptus globulus, Eucalyptus gomphocephala, Eucalyptus gunnii, Eucalyptus henryi, Eucalyptus laevopinea, Eucalyptus macarthurii, Eucalyptus macrorhyncha, Eucalyptus maculata, Eucalyptus marginata, Eucalyptus megacarpa, Eucalyptus melliodora, Eucalyptus nicholii, Eucalyptus nitens, Eucalyptus nova-anglica, Eucalyptus obliqua, Eucalyptus obtusiflora, Eucalyptus oreades, Eucalyptus pauciflora, Eucalyptus polybractea, Eucalyptus regnans, Eucalyptus resinifera, Eucalyptus robusta, Eucalyptus rudis, Eucalyptus saligna, Eucalyptus sideroxylon, Eucalyptus stuartiana, Eucalyptus tereticornis, Eucalyptus torelliana, Eucalyptus urnigera, Eucalyptus urophylla, Eucalyptus viminalis, Eucalyptus viridis, Eucalyptus wandoo, Eucalyptus youmanni.*

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction, and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the

present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. The preferred method for transforming eucalyptus and pine is a biolistic method using pollen (*see*, for example, Aronen, *Finnish Forest Res. Papers* 595:53, 1996) or easily regenerable embryonic tissues.

Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. For a review of regeneration of forest trees, *see* Dunstan *et al.*, *in* Thorpe TA, ed., *In vitro embryogenesis of plants, Current Plant Science and Biotechnology in Agriculture*, 20(12):471-540, 1995. Specific protocols for the regeneration of spruce are discussed by Roberts., Somatic embryogenesis of spruce," in Redenbaugh K, ed., *Synseed: applications of synthetic seed to crop improvement,* CRC Press: Ch. 23, pp. 427-449, 1993. The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

As discussed above, the production of RNA in target plant cells can be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target plant host. A target plant may be transformed with more than one genetic constructs of the present invention, thereby modulating the activity of more than one isoprenoid metabolism enzyme, affecting enzyme activity in more than one tissue, or affecting enzyme activity at more than one expression time. Similarly, a genetic construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme. The polynucleotides of the present inventive may also be employed in combination with other known sequences encoding enzymes involved in the synthesis of isoprenoids.

Additionally, the polynucleotides of the present invention have particular application for use as non-disruptive tags for marking organisms, particularly plants. Genetic constructs comprising polynucleotides of the present invention may be stably introduced into an organism as heterologous, non-functional, non-disruptive tags. It is then possible to identify the origin or source of the organism at a later date by determining the presence or absence of the tag(s) in a sample of material. Organisms other than plants may also be tagged with the polynucleotides of the present invention, including commercially valuable animals, fish, bacteria and yeasts.

Detection of the tag(s) may be accomplished using a variety of conventional techniques, and will generally involve the use of nucleic acid probes. Sensitivity in assaying the presence of probe can be usefully increased by using branched oligonucleotides, as described by Horn *et al., Nucleic Acids Res.* 25(23):4842-4849, 1997), enabling detection of as few as 50 DNA molecules in the sample.

The following examples are offered by way of illustration and not by way of limitation.

Example 1

Isolation and Characterization of cDNA Clones from *Pinus radiata* and *Eucalyptus grandis*

Pinus radiata and *Eucalyptus grandis* cDNA expression libraries were constructed and screened as follows. mRNA was extracted from the plant tissue using the protocol of Chang *et al., Plant Molecular Biology Reporter* 11:113-116, 1993 with minor modifications. Specifically, samples were dissolved in CPC-RNAXB (100 mM Tris-Cl, pH 8,0; 25 mM EDTA; 2.0 M NaCl; 2%CTAB; 2% PVP and 0.05% Spermidine*3HCl) and extracted with chloroform:isoamyl alcohol, 24:1. mRNA was precipitated with ethanol and the total RNA preparate was purified using a Poly(A) Quik mRNA Isolation Kit (Stratagene, La Jolla, CA). A cDNA expression library was constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA clones in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNAs were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 μl of sample DNA from the 5 μl ligation mix. Mass excision of the library was done using XL1-Blue MRF' cells and XLOLR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out

onto LB-kanamycin agar plates containing X-gal and isopropylthio-beta-galactoside (IPTG).

Of the colonies plated and picked for DNA miniprep, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and cDNA was purified by means of REAL DNA minipreps (Qiagen, Venlo, The Netherlands). Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a Biomek 2000 robot (Beckman Coulter Inc, Fullerton CA for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

Polynucleotides for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced first from the 5' end and, in some cases, also from the 3' end. For some clones, internal sequences were obtained using subcloned fragments. Subcloning was performed using standard procedures of restriction mapping and subcloning to pBluescript II SK+ vector and other standard sequencing vectors.

The determined cDNA sequences, including the polynucleotides of the present invention, were compared to and aligned with known sequences in the. Specifically, the polynucleotides identified in SEQ ID NOS. 1-53 were compared to polynucleotides in the EMBL database EMBL as of the end of August, 1998 using the BLASTN algorithm Version 2.0.4 [Feb-24-1998] set to the following running: Unix running command: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq –o results. The polynucleotides identified in SEQ ID NOS: 78-164 were compared to polynucleotides in the EMBL database EMBL as of the end of May, 1999 using BLASTN algorithm Version 2.0.6 [Sep-16-1998], set to the following running parameters: Unix running command: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq –o results. Multiple alignments of redundant sequences were used to build up reliable consensus sequences. Based on similarity to known sequences from other plant species, the isolated polynucleotides of the present invention identified as SEQ ID NOS. 1-53 and 78-164 were putatively identified as encoding polypeptides having similarity to the polypeptides shown above in Table 1.

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. The corresponding predicted

polypeptide sequences were determined and were compared to sequences in the SwissProt database using the computer algorithm BLASTP. Comparisons of DNA sequences provided in SEQ ID NOS: 78-164, to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NOS: 165-304 to sequences in the SwissProt database (using BLASTP) were made as of May, 1999. Analysis of six-frame translations of the polynucleotides of SEQ ID NOS: 78-164, were also compared to and aligned with the six-frame translations of polynucleotides in the EMBL database using the TBLASTX program.

BLASTN Polynucleotide Analysis

The cDNA sequences of SEQ ID NOS: 1, 2, 4-6, 8-12, 15, 19, 21-23, 27-33, 35, 37-42, 44, 46-52, 78-80, 82, 83, 86, 89-92, 96-100, 104-113, 115, 117, 120, 122-130, 132-136, 138-158, 160, 163 and 164, were determined to have less than 40% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The cDNA sequences of SEQ ID NOS: 3, 7, 14, 18, 20, 25, 34, 36, 53, 84, 85, 87, 88, 101, 114, 116, 118, 119, 131, 137, 159, 161 and 162 were determined to have less than 60% identity, determined as described above, to sequences in the EMBL database using BLASTN, as described above. The cDNA sequences of SEQ ID NOS: 16, 17, 26, 43, 45, 93, 94 and 121, were determined to have less than 75% identity, determined as described above, to sequences in the EMBL database using BLASTN, as described above. The cDNA sequences of SEQ ID NOS: 13, 24, 95, 102 and 103 were determined to have less than 90% identity, determined as described above, to sequences in the EMBL database using BLASTN, as described above.

BLASTP Amino Acid Analysis

The predicted amino acid sequences of SEQ ID NOS: 194-200, 202, 216, 223, 230, 235, 239, 240, 243, 250, 255, 259, 260, 263, 270, 272, 274, 278, 291, 292, 293, 296, 303 and 304 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the BLASTP computer algorithm as described above. The predicted amino acid sequences of SEQ ID NOS: 166, 168-177, 179, 183-188, 192, 203-205, 207, 209-213, 218, 219, 221, 224, 225, 227-229, 231, 232, 234, 237, 242, 244, 245, 251, 253, 262, 267, 268, 269, 273, 276, 277, 279, 281, 282, 284, 286, 289, 290, 294, 295, 297, 298, 299, 300, 301 and 302 were determined to have less

than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The predicted amino acid sequences of SEQ ID NOS: 165, 167, 178, 182, 189-191, 193, 201, 206, 208, 214, 215, 217, 220, 222, 226, 233, 238, 241, 246-250, 254, 256, 257, 258, 261, 264, 265, 266, 275, 280, 283, 285 and 288 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The predicted amino acid sequences of SEQ ID NOS: 180, 181 and 271, were determined to have less than 95% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

TBLASTX Analysis

The six-frame translations of the polynucleotide sequences of SEQ ID NOS: 78-164 were compared to and aligned with six-frame translations of polynucleotides in the EMBL database using the TBLASTX program version 2.0.6 [Sept-16-1998] set to the following running parameters: Unix running command: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -v 30 -b 30 -i queryseq –o results. The translations of the polynucleotides of SEQ ID NOS: 82, 83, 90, 107-113, 115, 120, 122, 124-126, 129, 134-136, 142-144, 146-149, 152, 153, 155-158 and 164, were determined to have less than 50% identity, determined as described above, to translations of polynucleotides in the EMBL database using the computer algorithm TBLASTX. The translations of the polynucleotides of SEQ ID NOS: 79, 81, 84-89, 91, 92, 96-101, 103, 105, 114, 116-118, 123, 131, 132, 137-141, 145, 150, 154 and 160-162, were determined to have less than 75% identity, determined as described above, to translations of polynucleotides in the EMBL database using the computer algorithm TBLASTX. The translations of the polynucleotide sequences of SEQ ID NOS: 78, 80, 93, 95, 102, 104, 106, 119, 121, 127, 128, 130, 133, 151, 159 and 163, were determined to have less than 90% identity, determined as described above, to translations of polynucleotides in the EMBL database using the computer algorithm TBLASTX. The translations of the polynucleotide sequence of SEQ ID NO: 94 was determined to have less than 95% identity, determined as described above, to translations of polynucleotides in the EMBL database using the computer algorithm TBLASTX.

Example 2

Use of an O-methyltransferase (OMT) Gene to Modify Lignin Biosynthesis

Transformation of tobacco plants with a *Pinus radiata* OMT gene

Genetic constructs comprising sense and anti-sense nucleotides containing a polynucleotide comprising the coding region of the enzyme O-methyltransferase (OMT) (SEQ ID NO: 54) from *Pinus radiata* were constructed and inserted into *Agrobacterium tumefaciens* by direct transformation using published methods (An *et al.*, "Binary vectors," *in* Gelvin SB and Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). General methods for plant transformation are described in Horsch et al., *Science* 227:1229-1231, 1985. The constructs of sense DNA were made by first cloning the PBK-CMV cDNA inserts into pART7 vectors. The pART7 vectors were then cut by restriction endonuclease *Not*I to remove the 35S-Insert-OCS 3'UTR construct for cloning into the plant expression vector pART27 (Gleave A, *Plant Mol. Biol.* 20:1203-1207, 1992). The presence and integrity of the transgenic constructs were verified by restriction digestion and DNA sequencing.

Tobacco (*Nicotiana tabacum* cv. Samsun) leaf sections were transformed with the sense and anti-sense OMT constructs using the method of Horsch *et al.*, *Science* 227:1229-1231, 1985. Five independent transformed plant lines were established for the sense construct and eight independent transformed plant lines were established for the anti-sense construct for OMT. Transformed plants containing the appropriate gene construct were verified using Southern blot experiments. A "+" in the column labeled "Southern" in Table 2 below indicates that the transformed plant lines were confirmed as independent transformed lines.

Expression of *Pinus* OMT in transformed plants

Total RNA was isolated from each independent transformed plant line created with the OMT sense and anti-sense constructs. The RNA samples were analyzed in Northern blot experiments to determine the level of expression of the transgene in each transformed line.

The data shown in the column labeled "Northern" in Table 1 shows that the transformed plant lines containing the sense and anti-sense constructs for OMT all exhibited high levels of expression, relative to the background on the Northern blots.

OMT expression in sense plant line number 2 was not measured because the RNA sample showed signs of degradation. There was no detectable hybridization to RNA samples from empty vector-transformed control plants.

Modulation of OMT enzyme activity in transformed plants

The total activity of OMT enzyme, encoded by the *Pinus* OMT gene and by the endogenous tobacco OMT gene, was analyzed for each transformed plant line created with the OMT sense and anti-sense constructs. Crude protein extracts were prepared from each transformed plant and assayed using the method of Zhang *et al.*, *Plant Physiol.* 113:65-74, 1997. The data contained in the column labeled "Enzyme" in Table 2 shows that the transformed plant lines containing the OMT sense construct generally had elevated OMT enzyme activity, with a maximum of 199%, whereas the transformed plant lines containing the OMT anti-sense construct generally had reduced OMT enzyme activity, with a minimum of 35%, relative to empty vector-transformed control plants. OMT enzyme activity was not estimated in sense plant line number 3.

Effects of *Pinus* OMT on lignin concentration in transformed plants

OMT is an enzyme involved in the biosynthesis of lignin. The concentration of lignin in the transformed tobacco plants was determined using the well-established procedure of thioglycolic acid extraction (Freudenberg *et al.*, *Constitution and Biosynthesis of Lignin*, Springer-Verlag: Berlin, 1968). Briefly, whole tobacco plants, of an average age of 38 days, were frozen in liquid nitrogen and ground to a fine powder in a mortar and pestle. 100 mg of frozen powder from one empty vector-transformed control plant line, the five independent transformed plant lines containing the sense construct for OMT and the eight independent transformed plant lines containing the anti-sense construct for OMT were extracted individually with methanol, followed by 10% thioglycolic acid and finally dissolved in 1 M NaOH. The final extracts were assayed for absorbance at 280 nm. The data shown in the column labeled "TGA" in Table 2 shows that the transformed plant lines containing the sense and the anti-sense OMT gene constructs all exhibited significantly decreased levels of lignin, relative to the empty vector-transformed control plant lines.

TABLE 2

plant line	transgene	orientation	Southern	Northern	Enzyme	TGA
1	control	na	+	blank	100	104
1	OMT	sense	+	2.9E+6	86	55
2	OMT	sense	+	na	162	58
3	OMT	sense	+	4.1E+6	na	63
4	OMT	sense	+	2.3E+6	142	66
5	OMT	sense	+	3.6E+5	199	75
1	OMT	anti-sense	+	1.6E+4	189	66
2	OMT	anti-sense	+	5.7E+3	35	70
3	OMT	anti-sense	+	8.0E+3	105	73
4	OMT	anti-sense	+	1.4E+4	109	74
5	OMT	anti-sense	+	2.5E+4	87	78
6	OMT	anti-sense	+	2.5E+4	58	84
7	OMT	anti-sense	+	2.5E+4	97	92
8	OMT	anti-sense	+	1.1E+4	151	94

These data clearly demonstrate that polynucleotides identified from isolated cDNA obtained as in Example 1 and encoding polypeptides, may be assembled in DNA constructs and used to transform plants. The data furthermore demonstrates that transformed plants comprising genetic constructs exhibit varied levels of such enzyme expression and activity, and that the modulation of the metabolism of such an enzyme, manipulated by either sense or anti-sense expression of a gene encoding the enzyme, such as OMT, affects end product concentrations, such as the lignin concentration in the transformed plants.

Example 3

Use of a 4-Coumarate:CoA ligase (4CL) Gene to Modify Lignin Biosynthesis

Transformation of tobacco plants with a *Pinus radiata* 4CL gene

Sense and anti-sense constructs containing a DNA sequence including the coding region of 4CL (SEQ ID NO: 55) from *Pinus radiata* were inserted into *Agrobacterium tumefaciens* LBA4301 by direct transformation as described above in Example 2. The presence and integrity of the transgenic constructs were verified by restriction digestion and DNA sequencing.

Tobacco (*Nicotiana tabacum* cv. Samsun) leaf sections were transformed as described above. Five independent transformed plant lines were established for the sense

construct and eight independent transformed plant lines were established for the anti-sense construct for 4CL. Transformed plants containing the appropriate lignin gene construct were verified using Southern blot experiments. A "+" in the column labeled "Southern" in Table 3 indicates that the transformed plant lines listed were confirmed as independent transformed lines.

Expression of *Pinus* 4CL in transformed plants

Total RNA was isolated from each independent transformed plant line created with the 4CL sense and anti-sense constructs. The RNA samples were analyzed in Northern blot experiments to determine the level of expression of the transgene in each transformed line. The data shown in the column labeled "Northern" in Table 3 below shows that the transformed plant lines containing the sense and anti-sense constructs for 4CL all exhibit high levels of expression, relative to the background on the Northern blots. 4CL expression in anti-sense plant line number 1 was not measured because the RNA was not available at the time of the experiment. There was no detectable hybridization to RNA samples from empty vector-transformed control plants.

Modulation of 4CL enzyme activity in transformed plants

The total activity of 4CL enzyme, encoded by the *Pinus* 4CL gene and by the endogenous tobacco 4CL gene in transformed tobacco plants, was analyzed for each transformed plant line created with the 4CL sense and anti-sense constructs. Crude protein extracts were prepared from each transformed plant and assayed using the method of Zhang *et al.*, *Plant Physiol.* 113:65-74, 1997. The data contained in the column labeled "Enzyme" in Table 2 shows that the transformed plant lines containing the 4CL sense construct had elevated 4CL enzyme activity, with a maximum of 258%, and the transformed plant lines containing the 4CL anti-sense construct had reduced 4CL enzyme activity, with a minimum of 59%, relative to empty vector-transformed control plants.

Effects of *Pinus* 4CL on lignin concentration in transformed plants

The concentration of lignin in samples of transformed plant material was determined as described in Example 2. The data shown in the column labeled "TGA" in Table 3, below, shows that the transformed plant lines containing the sense and the anti-sense 4CL gene constructs all exhibited significantly decreased levels of lignin, relative to

the empty vector-transformed control plant lines. These data demonstrate that the polynucleotides identified from isolated cDNA as obtained in Example 1 may be assembled into DNA constructs and used to transform plants. Transformed plants comprising such genetic constructs exhibit modified levels of enzyme expression and activity. The metabolism of the biosynthetic pathway involving the enzyme is also affected.

TABLE 3

plant line	transgene	orientation	Southern	Northern	Enzyme	TGA
1	control	na	+	blank	100	92
2	control	na	+	blank	100	104
1	4CL	sense	+	2.3E+4	169	64
2	4CL	sense	+	4.5E+4	258	73
3	4CL	sense	+	3.1E+4	174	77
4	4CL	sense	+	1.7E+4	164	80
5	4CL	sense	+	1.6E+4	184	92
1	4CL	anti-sense	+	na	59	75
2	4CL	anti-sense	+	1.0E+4	70	75
3	4CL	anti-sense	+	9.6E+3	81	80
4	4CL	anti-sense	+	1.2E+4	90	83
5	4CL	anti-sense	+	4.7E+3	101	88
6	4CL	anti-sense	+	3.9E+3	116	89
7	4CL	anti-sense	+	1.8E+3	125	94
8	4CL	anti-sense	+	1.7E+4	106	97

Example 4

Transformation of Tobacco using Lignin Biosynthetic Genes

Sense and anti-sense constructs containing DNA sequences including the coding regions of coumarate 3-hydroxylase (C3H) (SEQ ID NO: 56), ferulate-5-hydroxylase (F5H) (SEQ ID NO: 57), cinnamoyl-CoA reductase (CCR) (SEQ ID NO: 58) and coniferyl glycosyl transferase (CGT) (SEQ ID NO: 59) from *Eucalyptus grandis*, and phenylalanine ammonia-lyase (PAL) (SEQ ID NOS: 60 and 61), cinnamate 4-hydroxylase (C4H) (SEQ ID NOS: 62 and 63), phenolase (PNL) (SEQ ID NO: 64) and laccase (LAC) (SEQ ID NO: 65) from *Pinus radiata* were inserted into *Agrobacterium tumefaciens* LBA4301 by direct transformation as described above. The presence and

integrity of the transgenic constructs were verified by restriction digestion and DNA sequencing.

Tobacco (*Nicotiana tabacum* cv. Samsun) leaf sections were transformed as described in Example 2. Up to twelve independent transformed plant lines were established for each sense construct and each anti-sense construct listed in the preceding paragraph. Transformed plants containing the appropriate lignin gene construct were verified using Southern blot experiments. All of the transformed plant lines analyzed were confirmed as independent transformed lines. This demonstrates that transgenic plants with an expressed novel gene can be made, starting the whole process from an isolated cDNA obtained as in Example 1.

Example 5

Manipulation of Lignin Content in Transformed Plants

Determination of transgene expression by Northern blot experiments

Total RNA was isolated from each independent transformed plant line described in Example 4. The RNA samples were analyzed in Northern blot experiments to determine the level of expression of the transgene in each transformed line. The column labeled "Northern" in Table 4 shows the level of transgene expression for all plant lines assayed, relative to the background on the Northern blots. There was no detectable hybridization to RNA samples from empty vector-transformed control plants.

Determination of lignin concentration in transformed plants

The concentration of lignin in empty vector-transformed control plant lines and in up to twelve independent transformed lines for each sense construct and each anti-sense construct described in Example 5 was determined as described in Example 3. The column labeled "TGA" in Table 3 shows the thioglycolic acid extractable lignins for all plant lines assayed, expressed as the average percentage of TGA extractable lignins in transformed plants versus control plants. The range of variation is shown in parentheses.

TABLE 4

transgene	orientation	no. of lines	Northern	TGA
control	na	3	blank	100 (92-104)
C3H	sense	5	3.7E+4	74 (67-85)
F5H	sense	10	5.8E+4	70 (63-79)
F5H	anti-sense	9	5.8E+4	73 (35-93)
CCR	sense	1	na	74
CCR	anti-sense	2	na	74 (62-86)
transgene	orientation	no. of lines	Northern	TGA
PAL	sense	5	1.9E+5	77 (71-86)
PAL	anti-sense	4	1.5E+4	62 (37-77)
C4H	anti-sense	10	5.8E+4	86 (52-113)
PNL	anti-sense	6	1.2E+4	88 (70-114)
LAC	sense	5	1.7E+5	na
LAC	anti-sense	12	1.7E+5	88 (73-114)

Transformed plant lines containing the sense and the anti-sense lignin biosynthetic gene constructs all exhibited significantly decreased levels of lignin, relative to the empty vector-transformed control plant lines. The most dramatic effects on lignin concentration were seen in the F5H anti-sense plants with as little as 35% of the amount of lignin in control plants, and in the PAL anti-sense plants with as little as 37% of the amount of lignin in control plants. These data clearly indicate that the concentration of a polynucleotide, such as lignin, as measured by the TGA assay, can be directly manipulated by conventional anti-sense methodology and also by sense over-expression using the inventive lignin biosynthetic genes, starting the whole process from an isolated cDNA obtained as in Example 1.

Example 6

Modulation of Lignin Enzyme Activity in Transformed Plants

The activities and substrate specificities of selected lignin biosynthetic enzymes were assayed in crude extracts from transformed tobacco plants containing sense and anti-sense constructs for PAL (SEQ ID NO: 60), PNL (SEQ ID NO: 64) and LAC (SEQ ID NO: 65) from *Pinus radiata*, and CGT (SEQ ID NO: 59) from *Eucalyptus grandis*.

Enzyme assays were performed using published methods for PAL (Southerton SG and Deverall BJ, *Plant Path.* 39:223-230, 1990); CGT (Vellekoop *et al.*, *FEBS Lett.*

330:36-40, 1993); PNL (Espin *et al.*, *Phytochemistry* 44:17-22, 1997); and LAC (Bao *et al.*, *Science* 260:672-674, 1993). The data shown in the column labelled "Enzyme" in Table 5 shows the average enzyme activity from replicate measures for all plant lines assayed, expressed as a percent of enzyme activity in empty vector-transformed control plants. The range of variation is shown in parentheses.

TABLE 5

Transgene	orientation	no. of lines	enzyme	
control	na	3	100	
PAL	sense	5	87	(60-124)
PAL	anti-sense	3	53	(38-80)
CGT	anti-sense	1	89	
PNL	anti-sense	6	144	(41-279)
LAC	sense	5	78	(16-240)
LAC	anti-sense	11	64	(14-106)

All of the transformed plant lines, except the PNL anti-sense transformed plant lines, showed average enzyme activities that were significantly lower than the activities observed in empty vector-transformed control plants. The most dramatic effects on lignin enzyme activities were seen in the PAL anti-sense transformed plant lines, in which all of the lines showed reduced PAL activity, and in the LAC anti-sense transformed plant lines, which showed as little as 14% of the LAC activity in empty vector-transformed control plant lines. These results demonstrate that enzyme activity can be modulated by transforming plants with polynucleotides encoding an enzyme of interest, starting the whole process from polynucleotides encoding enzymes of interest isolated from cDNA as described in Example 1.

Example 7

Functional Identification of Lignin Biosynthetic Genes

Sense constructs containing DNA sequences including the coding regions for PAL (SEQ ID NO: 61), OMT (SEQ ID NO: 54), 4CL (SEQ ID NOS: 55 and 66) and POX (SEQ ID NO: 67) from *Pinus radiata*, and OMT (SEQ ID NOS: 68 and 69), CCR (SEQ ID NOS: 70 - 72), CGT (SEQ ID NOS: 59 and 73) and POX (SEQ ID NOS: 74 and 75)

from *Eucalyptus grandis* were inserted into the commercially available protein expression vector, pProEX-HT (Gibco BRL). The resultant constructs were transformed into *E. coli* XL1-Blue (Stratagene), which were then induced to produce recombinant protein by the addition of IPTG. Purified proteins were produced for the *Pinus* OMT and 4CL constructs and the *Eucalyptus* OMT and POX constructs using Ni column chromatography (Janknecht *et al.*, *Proc. Natl. Acad. Sci. USA* 88:8972-8976, 1991). Enzyme assays for each of the purified proteins conclusively demonstrated the expected substrate specificity and enzymatic activity for the genes tested.

The data for two representative enzyme assay experiments, demonstrating the verification of the enzymatic activity of a *Pinus radiata* 4CL gene (SEQ ID NO: 55) and a *Pinus radiata* OMT gene (SEQ ID NO: 54), are shown below in Table 6. For the 4CL enzyme, one unit equals the quantity of protein required to convert the substrate into product at the rate of 0.1 absorbance units per minute. For the OMT enzyme, one unit equals the quantity of protein required to convert 1 pmole of substrate to product per minute.

TABLE 6

transgene	purification step	total ml extract	total mg protein	total units activity	% yield activity	fold purification
4CL	crude	10 ml	51 mg	4200	100	1
	Ni column	4 ml	0.84 mg	3680	88	53
OMT	crude	10 ml	74 mg	4600	100	1
	Ni column	4 ml	1.2 mg	4487	98	60

The data shown in Table 6 demonstrate that both the purified 4CL enzyme and the purified OMT enzyme show high activity in enzyme assays, confirming the identification of the 4CL and OMT genes. Crude protein preparations from *E. coli* transformed with empty vector show no activity in either the 4CL or the OMT enzyme assay. This demonstrates that the function of an isolated novel cDNA with only a putative function can be confirmed, starting the whole process from an isolated cDNA obtained as in Example 1.

Example 8

Demonstration of the Presence / Absence of Unique Sequence Identifiers in Plants

Transgenic tobacco plants were created using unique identifier sequences which are not found in tobacco. The unique identifier sequences inserted were isolated from *Pinus radiata*, SEQ ID NO: 76, and *Eucalyptus grandis*, SEQ ID NO: 77. The unique identifier sequences were inserted into *Agrobacterium tumefaciens* LBA4301 (provided as a gift by Dr. C. Kado, University of California, Davis, CA) by direct transformation using published methods (An *et al.*, "Binary vectors," *in* Gelvin SB and Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the unique identifier sequences in the *Agrobacterium* transgenic constructs were verified by restriction digestion and DNA sequencing.

Tobacco (*Nicotiana tabacum* cv. Samsun) leaf sections were transformed using the method of Horsch *et al.*, *Science* 227:1229-1231, 1985. Three independent transformed plant lines were established for each unique sequence identifier used. Two empty-vector control plant lines were established using an empty gene transfer vector that lacked a unique sequence identifier.

The uniqueness of the sequence identifiers was assayed using Southern blot analyses to test for the presence of the sequence identifier in the genome of the plants. If the sequence identifier is unique and therefore useful as a tag, then the sequence identifier should be clearly absent in plants which have not been tagged and it should be clearly present in plants which have been tagged. In the present example, the unique identifiers would be expected to be absent in the empty-vector transformed control plants. The unique identifier would be expected to be present in the transgenic plants transformed with the unique sequence identifiers.

Genomic DNA was prepared from empty-vector transformed control plants and plants transformed with unique sequence identifiers using the cetyltrimethyl-ammonium bromide (CTAB) extraction method of Murray MG and Thompson WF, *Nucleic Acids Res.* 8:4321-4325, 1980. The DNA samples were digested with the restriction enzyme *Eco*RI in the case of the plants transformed with the *Pinus* unique sequence identifier (SEQ ID NO: 76) and the restriction enzyme *Xba*I in the case of the plants transformed with the *Eucalyptus* unique sequence identifier (SEQ ID NO: 77). The DNA fragments

produced in the restriction digests were resolved on a 1% agarose gel; the left panel of Fig. 2 and the right panel of Fig. 2 show the DNA fragment patterns of the DNA samples from the *Pinus* and *Eucalyptus* experiments, respectively.

After the agarose gel electrophoresis step, the DNA samples were transferred to Hybond-N+ nylon membranes (Amersham Life Science, Little Chalfont, Buckinghamshire, England) using methods established by Southern, *J. Mol. Biol.* 98:503-517, 1975. The nylon membranes were probed with radioactively-labeled probes for the unique sequence identifiers identified above and washed at high stringency (final wash: 0.5 X salt sodium citrate buffer (SSC) plus 0.1% sodium dodecyl sulfate (SDS), 15 minutes at 65°C). The hybridization of the probes to complementary sequences in the genomic DNA samples was detected using auto-radiography.

The results are shown in Figs. 3 and 4.

Fig. 3 (corresponding to the left panel of Fig. 2) shows the hybridization pattern detected in the Southern blot analysis using a probe derived from the *Pinus* sequence identifier (SEQ ID NO: 76). Lanes A-B contain DNA samples from empty-vector transformed control plants and Lanes C-E contain DNA from plants transformed with SEQ ID NO: 76. There is no hybridization in Lanes A-B indicating that SEQ ID NO: 76 is not present in empty-vector transformed tobacco plants; that is, SEQ ID NO: 76 is a unique tag suitable for unambiguous marking of tobacco plants. There is strong hybridization in Lanes C-E, indicating that the plants which received SEQ ID NO: 76 via transformation have been clearly and unambiguously tagged with the unique sequence contained in SEQ ID NO: 76.

Fig. 4 (corresponding to the right panel of Fig. 2) shows the hybridization pattern detected in the Southern blot analysis using a probe derived from the *Eucalyptus* sequence identifier (SEQ ID NO: 77). Lanes A-B contain DNA samples from empty-vector transformed control plants and Lanes C-E contain DNA from plants transformed with SEQ ID NO: 77. There is no hybridization in Lanes A-B indicating that SEQ ID NO: 77 is not present in empty-vector transformed tobacco plants; that is, SEQ ID NO: 77 is a unique tag suitable for unambiguous marking of tobacco plants. There is strong hybridization in Lanes C-E indicating that the plants which received SEQ ID NO: 77 via transformation have been clearly and unambiguously tagged with the unique sequence contained in SEQ ID NO: 77.

The data clearly demonstrates the utility of the sequences disclosed in this specification for the purposes of unambiguously tagging transgenic materials. A unique sequence was selected from a large number of potential tags and shown to be absent in the genome of the organism to be tagged. The tag was inserted into the genome of the organism to be tagged and a well-established DNA detection method was used to clearly detect the unique sequence identifier used as the tag.

Because of the sequence-specific detection methods used in the example, a user of the invention disclosed in this specification has both a high likelihood of finding a sequence identifier, among the list which has been disclosed, which will be useful for tagging any given organism and an unequivocal method for demonstrating that a tagged organism could only have acquired a given tag through the deliberate addition of the unique sequence to the genome of the organism to be tagged. If the user of this invention maintains the precise sequence of the tag used in a given organism as a secret, then any disputes as to the origin and history of the organism can be unambiguously resolved using the tag detection techniques demonstrated in the present example.

SEQ ID NOS: 1-304 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties. While in the foregoing specification, this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

Claims:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of: (1) the sequences recited in SEQ ID NOS: 1-53 and 78-164; (2) complements of the sequences recited in SEQ ID NOS: 1-53 and 78-164; (3) reverse complements of the sequences recited in SEQ ID NOS: 1-53 and 78-164; (4) reverse sequences of the sequences recited in SEQ ID NOS: 1-53 and 78-164; (5) sequences comprising a polynucleotide sequence having at least 40% identity to a compare sequence selected from the polynucleotide sequences recited in SEQ ID NOS: 1, 2, 4-6, 8-12, 19, 21-23, 28-33, 35, 37-42, 44, 46-52, 78-80, 82, 83, 86, 89-92, 96-100, 104-113, 115, 117, 120, 122-130, 132-136, 138-158, 160, 163 and 164, the percentage identity determined by aligning the sequence and the compare sequences using the BLASTN algorithm version 2.04 set at the parameter values described herein, identifying the number of identical nucleic acids over aligned portions of the sequence and the compare sequences, dividing the number of identical nucleic acids by the total number of nucleic acids of the compare sequence, and multiplying by 100 to determine the percentage identity; (6) sequences comprising a polynucleotide sequence having at least 60% identity to a compare sequence selected from the polynucleotide sequences recited in SEQ ID NOS: 3, 7, 14, 18, 20, 25, 34, 36, 53, 84, 85, 87, 88, 101, 114, 116, 118, 119, 131, 137, 159, 161 and 162, the percentage identity determined as described in (5) above; (7) sequences comprising a polynucleotide sequence having at least 75% identity to a compare sequence selected from the polynucleotide sequences recited in SEQ ID NOS: 16, 17, 26, 43, 45, 93, 94 and 121, the percentage identity determined as described in (5) above; (8) sequences comprising a polynucleotide sequence having at least 90% identity to a compare sequence selected from the nucleotide sequences recited in SEQ ID NOS: 13, 24, 95, 102 and 103, the percentage identity determined as described in (5) above; (9) sequences comprising a polynucleotide sequence that hybridizes to a polynucleotide comprising a sequence recited in (1) – (8) above under stringent hybridization conditions; (10) sequences comprising a polynucleotide sequence that is a 100-mer of a sequence recited in (1) – (8) above; (11) sequences comprising a polynucleotide sequence that is a 40-mer of a sequence recited in (1) – (8) above; and (12) sequences

comprising a polynucleotide sequence that is a 20-mer of a sequence recited in (1) – (8) above; and (13) sequences comprising a polynucleotide sequence differing from a sequence recited in (1) – (12), above, only by one or more conservative substitutions.

2. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in Claim 1.

3. A genetic construct comprising a polynucleotide described in claim 1.

4. A transgenic cell comprising a genetic construct according to claim 3.

5. A transgenic cell according to claim 4, wherein the cell is selected from one of the following: a bacterial cell; an insect cell; a yeast cell; a mammalian cell; and a plant cell.

6. A genetic construct comprising, in the 5'-3' direction:

   (a) a gene promoter sequence;

   (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide comprising a nucleotide sequence of claim 1 coding for at least a functional portion of an enzyme having activity in an isoprenoid biosynthetic pathway; and (2) a polynucleotide comprising nucleotide sequence of claim 1 that includes a non-coding region of a polynucleotide encoding an enzyme having activity in an isoprenoid biosynthetic pathway; and

   (c) a gene termination sequence.

7. The construct of claim 6 wherein the polynucleotide is in a sense orientation.

8. The construct of claim 6 wherein the polynucleotide is in an antisense orientation.

9. The construct of claim 6 wherein the gene promoter sequence and gene termination sequences are functional in a plant host.

10. A transgenic cell comprising a construct of claim 6.

11. The transgenic cell of claim 10 wherein the polynucleotide is in a sense orientation.

12. The transgenic plant cell of claim 10 wherein the polynucleotide is in an antisense orientation.

13. A transgenic cell according to claim 10, wherein the cell is selected from one of the following: a bacterial cell; an insect cell; a yeast cell; a mammalian cell; and a plant cell.

14. A plant comprising a transgenic cell according to claim 9, or fruit or seeds or progeny thereof.

15. The plant of claim 14 wherein the plant is a woody plant.

16. The plant of claim 15 wherein the plant is selected from the group consisting of eucalyptus and pine species.

17. A method for modulating one or more of the content, the composition, and the metabolism of an enzyme involved in an isoprenoid biosynthetic pathway in an organism, comprising stably incorporating into the genome of the organism a construct of claim 3.

18. A method according to claim 17, wherein the organism is a plant.

19. A method for modulating one or more of the content, the composition, and the metabolism of an isoprenoid compound in an organism comprising stably incorporating into the genome of the organism a construct of claim 6.

20. A method according to claim 19, wherein the organism is a plant.

21. A method for producing an organism having one or more of altered isoprenoid content, altered isoprenoid composition and altered isoprenoid metabolism, comprising:

    (a) transforming a host cell with a construct of claim 3 to provide a transgenic host cell; and

    (b) cultivating the transgenic host cell under conditions conducive to growth and regeneration.

22. A method according to claim 21, wherein the organism is a plant and the host cell is a plant cell.

23. An isolated polypeptide encoded by a polynucleotide of claim 1.

24. A polypeptide of claim 23 having enzymatic activity in an isoprenoid biosynthetic pathway in a plant.

25. An isolated polypeptide comprising an amino acid sequence expressed from a polynucleotide that hybridizes to a nucleotide sequence set forth as SEQ ID NOS: 1-53 and 78-164 under stringent hybridization conditions.

26. An isolated polypeptide comprising a polypeptide sequence selected from the group consisting of: (1) the sequences set forth in SEQ ID NOS: 165-286 and 288-304; (2) sequences comprising a polypeptide sequence having at least 50% identity to a compare sequence selected from the polypeptide sequences recited in SEQ ID NOS: 194-200, 202, 216, 223, 230, 235, 239, 240, 243, 250, 255, 259, 260, 263, 270, 272, 274, 278, 291, 292, 293, 296, 303 and 304; (3) sequences comprising a polypeptide sequence having at least 75% identity to a compare sequence selected from the polypeptide sequences recited in SEQ ID NOS: 166, 168-177, 179, 183-188, 192, 203-205, 207, 209-213, 218, 219, 221, 224, 225, 227-229, 231, 232, 234, 237, 242, 244, 245, 251, 253, 262, 267, 268, 269, 273, 276, 277, 279, 281, 282, 284, 286, 289, 290, 294, 295, and 297-302; (4) sequences comprising a polypeptide sequence having at least 90% identity to a compare sequence selected from the polypeptide sequences recited in SEQ ID NOS: 165, 167, 178, 182, 189-191, 193, 201, 206, 208, 214, 215, 217, 220, 222, 226, 233, 238, 241, 246-250, 254, 256-258, 261, 264, 265, 266, 275, 280, 283, 285 and 288; (5) sequences comprising a polypeptide sequence having at least 95% identity to a compare sequence selected from the polypeptide sequences recited in SEQ ID NOS: 180, 181 and 271; (6) sequences comprising a polypeptide sequence that is a 100-mer of a sequence recited in (1) – (5) above having at least 100 residues; (7) sequences comprising a polypeptide sequence that is a 40-mer of a sequence recited in (1) – (5) above having at least 40 residues; and (8) sequences comprising a polypeptide sequence that is a 20-mer of a sequence recited in (1) – (5) above.

27. A method for modulating one or more of the content, the composition and the metabolism of an isoprenoid compound in an organism, comprising administering an isolated polypeptide of claim 26 to the organism.

28. A method according to claim 27, wherein the organism is a plant, and administration of the isolated polypeptide is topical.

29. A method according to claim 27, wherein the organism is a mammal, and administration of the isolated polypeptide is systemic.

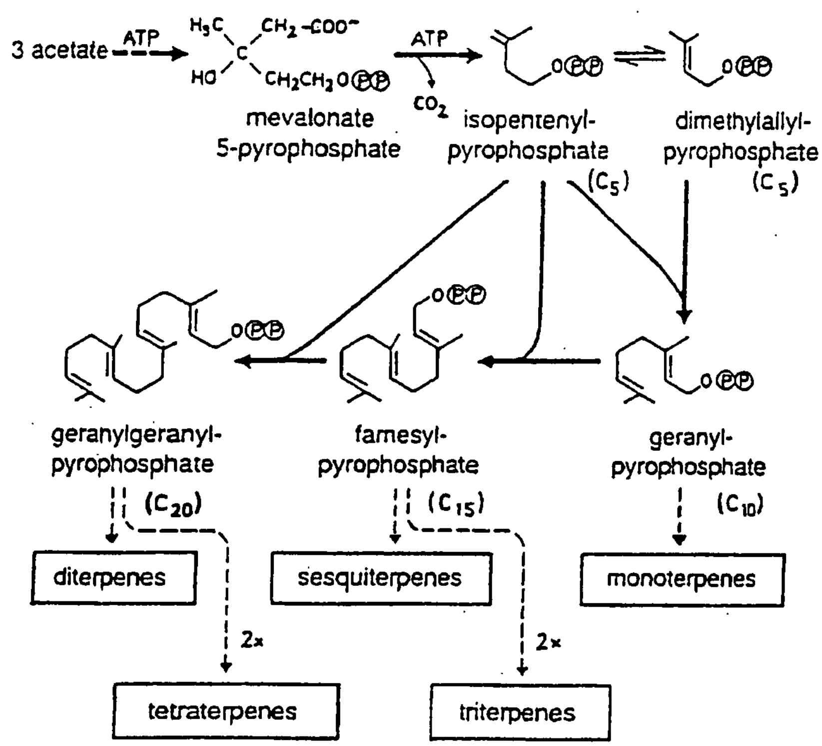
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FIGURE 1

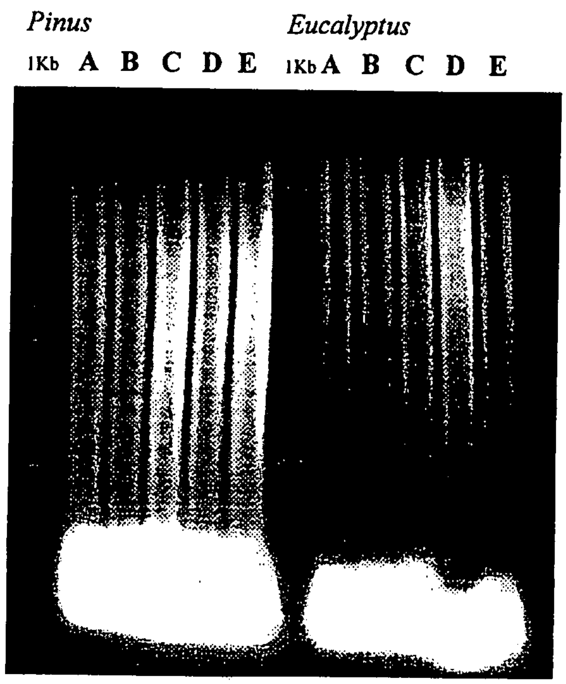

FIGURE 2

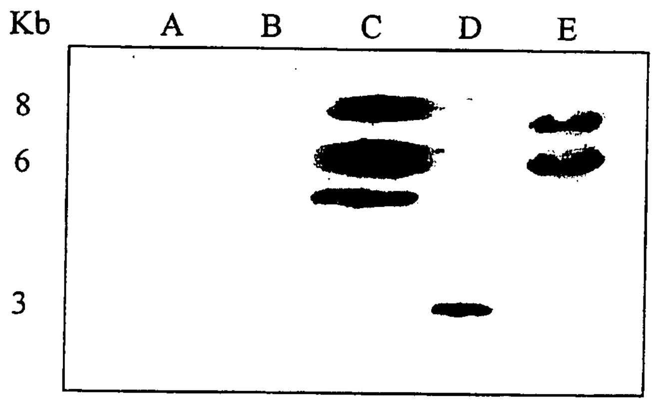

FIGURE 3

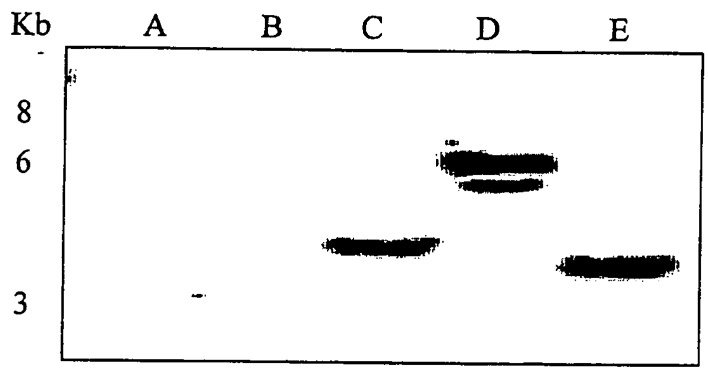

FIGURE 4

SEQUENCE LISTING

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ctacttcgta atcatattcc acgaatcctt aagaatcact tccgtgggaa gccttactat 540
gtagatctgc tg 552

<210> 4
<211> 371
<212> DNA
<213> Eucalyptus grandis

<400> 4
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ggcgttcgag ttttccgatg attcccgcca gtgggtcgaa cgggagaact atgggaaacc 240
tgattcagca aatgtcgcaa aagtgaaagt cctctaccac gagatcaatc ttcagggata 300
ctgcaagagc atttcaaaga acaagaacat tccgacggtg aaggcaaatg caaattcggt 360
tgaagcaacc a 371

<210> 5
<211> 408
<212> DNA
<213> Pinus radiata

<400> 5
agaccttgcc atctggaatg gattcacatt cataagactg cagtgatctt ggagtgctca 60
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tatgcccgta gcgtggggct tctgtttcag gttgtcgatg acatactcga tgtcacgaaa 180
tcatcaaaag aattgggcaa aactgcagga aaggatttga ttactgacaa ggccacttat 240
cccaagctga tgggtttaga gacagcaaag caatttgctg tcgagttgtt gggcagagct 300
aaggaagatt tatcttgctt cgacccaaag aaggccgcac cgttgttggg tattgcagag 360
tacattgcat tcagacaaaa ctgaaaagtc tcctaaaagt gtcttacg 408

<210> 6
<211> 590
<212> DNA
<213> Eucalyptus grandis

<400> 6
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ctgttgttct tggggcaatt atgggaggtg ggtctaatga agaagttgag aagttgcggg 420
gttttgcaag gtgtattggg ttgttatttc aagtggtgga tgatattctg gatctgaccc 480
agtcttctca agaactgggt aaaacggctg gcaaggattt ggtggctgac aaagttacgt 540
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<210> 7
<211> 699
<212> DNA
<213> Eucalyptus grandis

<400> 7
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tctggttttt caccacattc ggtctccgtc tccctccgat ctcgagttca gcaagcgaga 180
gagagagaga gagagagaga gagagagaga gagagagaga aatggggagt ttgggagcca 240
tcctgaagca cccggacgat ttctacccgc tgctgaagct gaagatcgcg gcaaggaatg 300
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gcatatttta tttggtcctg cgagcacttg atacagttga ggatgacaca agcatacctа 480
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atttttcatg cggtacaaaa gagtacaagg ttctaatgga ccaatttcat catgtttcaa 600
ctgctttcct ggagctgggg aaaagttacc aagaggcaat tgatgatatt actaaaagaa 660
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<210> 8
<211> 373
<212> DNA
<213> Pinus radiata

<400> 8
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gtggcgattg cggtagccat tggctttgtt tctgtattat tgtcgtatta tatagttttg 180
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tcaacagatg acaatggcat tgccatcgaa gctgctggag gaacggatgt tatcatcgtg 300
ggagcaggag tcgcgggttc ggctctggct tacacacttg gcaaggatgg aagacgtata 360
catgtaattg aga 373

<210> 9
<211> 373
<212> DNA
<213> Pinus radiata

<400> 9
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atcgactgat atcgtggtct acaatggaga atcatacggt ggtgattgcg gcagccatta 180
gctttgtttc tgtattattg tcgtattata tagttttgag caggtggaag cgcagatcca 240
acggattacg gggaatacag agcaaaagtt tcgaaaagtc aacagatgac aatggcattg 300
ccatcgaagc tgctggagga acggatgtta tcatcgtggg agcaggagtc gcgggttcgg 360
ctctggctta cac 373

<210> 10
<211> 825
<212> DNA
<213> Eucalyptus grandis

<400> 10
ccctcaattg tacaaagcct tcatcgcagc aattgacaag ggaaacatca agtcgatgcc 60
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gttcaacatg cgccatccat tgacaggagg aggaatgacc gtggctcttt ctgatatcgt     180
tttgctaagg aacctccttc gcccacttca ggatctgaat gatgcatctg ctctatgcaa     240
atatctcgag tcgttctata cactgaggaa gcctgtggcg tcgaccatca acaccctggc     300
tggtgctctg tacaaggtct tctgtgcatc tccagacccg gcaagaaagg aaatgcgcca     360
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gatgttcttc cctgcgactg tgccggctta ccacagagct cctcctgttc actgagagaa     660
tgcagcaaag ctcgataagc gcatgaatat gcggtcaagt tcgtttcttc tagtcacatt     720
cctctctcgt agtagatgga gaggcctgcc agttatactg cactcggaag agaattgtgc     780
attggaacta tagatttcgt tacgataagt agattcattc aagaa                     825
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<210> 11
<211> 394
<212> DNA
<213> Eucalyptus grandis

<400> 11

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atcgagatcg gggcttctt tacgattcag atccgtcgtc ttcatcgctc tccccgccgc     180
ggccgttcgc gctcaccttc ttcgacaggg agaggcacgt gacgttcctg gagatgatgt     240
accacatgct ccctcgcccc taccagtcgc aggagatcaa ccacctcacc ctcgcctact     300
tcgtcatctc cggcctcgac atcctcgacg ccctcgatcg cgtacacaaa gatgcggttg     360
ctgactgggt tttatctttc caagctcatt tcga                                 394
```

<210> 12
<211> 245
<212> DNA
<213> Eucalyptus grandis

<400> 12

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gagatactca ccaaagtgat ctccctcgct tccattatgg acgatatcta cgatgtctat      60
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atggatggat taccagagta tatgcaagct tatttcaagg agtttctcca gctctatgaa     180
tatattggga atcaattggc cgcaaaagga agatcgtacc gccttatcta cgcaaaagaa     240
gtgat                                                                 245
```

<210> 13
<211> 375
<212> DNA
<213> Pinus radiata

<400> 13

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ttatatcggg cttccctcat tgcctttcca ggagagaaag tcatggatga ggctgaaact      60
ttctctgcga aatatttgaa agaagccctg caaaagattc cagtctccag tctttcacga     120
gagatagggg acgtcctcga gtatggttgg cacacgtatt tgccacgatt ggaagcaagg     180
aattacatcg acgtcttcgg acaggacact gaaaacagca agtcatatat gaagaccgag     240
aaacttctcg aacttgcaaa gttggagttc aacatctttc acgccttaca aaagcgagag     300
ttggaatatc tcgtgagatg gtggaaaggc tctggttcgc ctcaaatgac cttttgtcga     360
catcgtcacg tggag                                                      375
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<210> 14
<211> 824
<212> DNA
<213> Pinus radiata

<400> 14

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aaatgccaca agatatgaaa atatgtttta agggttttta caatactttt aatgaaatcg      60
ctgaagaagg gcgaaaaagg caggggcgtg atgtgctaag ttacattcaa aaagtttggg     120
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```
aagtccagct agaagcatat accaaagaag cagaatggtc tgcagtgaga tacgtgccat    180
cctatgatga atatataggg aacgcgagtg tttcaatagc attgggaaca gtggttctta    240
tcagcgctct ttttactggg gagattctta cagatgacat actctccaaa attggtcgcg    300
attccagatt tctatacctc atgggcttga cagggcgtct cgtgaacgac accaaaactt    360
atcaggctga gagaggtcaa ggagaggtgg cttctgcagt acaatgttac atgaaggacc    420
atcctgagat ctccgaagaa gaagctctca aacatgtcta tactatcatg gataatgctc    480
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gttgcttact attggtattt gtaagacctg tcttgtttgt ttagcacaag ccatgaggtg    780
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```

<210> 15
<211> 1271
<212> DNA
<213> Eucalyptus grandis

<400> 15

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atcaagtcgg tcgtcgaggg aaagatgccg tcgtactcgc tcgagtccaa gcttggggac    180
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gagtactcgg tcccgatggc gaccaccgag ggtgtttgg tggcgagcac gaacaggggc     420
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gcgggagcca actcgaggct cctggccacg gtcgtgtccg gcgccgtcct tgccgccgag   1260
ctctcctcat g                                                         1271
```

<210> 16
<211> 372
<212> DNA
<213> Pinus radiata

<400> 16

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ttggcctcct cgtgcgtgtc caaatctttg atcagttctg ttcgtgagca taaggctctc    120
cgcagagcaa tcgcaacact gcaaatgtct aggccaggaa aatctgtggc ggcttccacc    180
aggatgagtt cggccactgc cggatctgat gatggcgtaa aaaggcgcat aggcgattat    240
cattctaacc tgtgggagga caattttata caatctctct catcacctta tggggcatct    300
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tcgattgcag at                                                        372
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<210> 17
<211> 520
<212> DNA
<213> Pinus radiata

<400> 17
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ccgtgtccaa atctttgatc agttctgttc gtgagcataa ggctctccgc agagcaatcg 120
caacactgca aatgtctagg ccaggaaaat ctgtggcggc ttccaccaag atgagttcgg 180
ccactgccgg atctgatgat ggtgtaaaaa ggcgcatagg cgattatcat tctaacctgt 240
gggacgacaa tgtcatacaa tctctctcat caccttatgg ggcatcttcg tacggtgagc 300
atgctgacag acttattggg gaagtgaagg agattttcaa ctcattttcg attgcagatg 360
gagaattaac cagtcctgtc aatgatctcc ttcaacagct ctggatggtc gataatgttg 420
aacgtttggg gatcgacaga catttccaaa ctgaaataaa agttgctctt gactatggtt 480
acagatattg gagcgaaaaa ggcattgaat gtggggagag 520

<210> 18
<211> 435
<212> DNA
<213> Pinus radiata

<400> 18
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gtgggatgat aatttcataa aatctctctc gtcaccttat ggggcatctt cgtaccgtga 180
gcatgctgac agagttattg gtgaagtaaa ggagattttc aactcacttt cgatgacaga 240
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tgagcgtttg gggatcgaca gacatttcca gaccgagata aaacttactc ttgactatgt 360
ttacagttat tggagcgaaa aaggcattgg atatgggaga gagagcgcta ttactgatct 420
caacacaact tccct 435

<210> 19
<211> 320
<212> DNA
<213> Pinus radiata

<400> 19
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caccgataaa tctaggggtt ttaatgttct cagagacgtg tccatgccac aaataatgat 120
aaagtcctgc aaagtgtctc cagacgcgcg gccataccaa aacctgggcg gtccagcgtc 180
ctcggaacgg ccattcttgg ctttctttgc aggccaaatg cacgggactc tgaggcccga 240
aattctcaag cactggggaa acgaaacaga tcctaacatg aaaatctttg cggtgggcca 300
gtcacatccc ggatcactac 320

<210> 20
<211> 626
<212> DNA
<213> Eucalyptus grandis

<400> 20
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tgggcccccct ggagccctcg gctcgtggag gcggtcgtgt tcggctgcat ccccgtgatc 180
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ttatgtacca tgcaaaatga tgtacc 626

<210> 21
<211> 490
<212> DNA
<213> Eucalyptus grandis

<400> 21
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ccgcgggtta tcaccccagc gtatgggggg actacttcct taaatatgat tctccctcca 180
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tctttgacaa 490

<210> 22
<211> 396
<212> DNA
<213> Eucalyptus grandis

<400> 22
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ttgctgagcc tatatgaagc ttgccattta aggtgtcatg gcgattcaat cttggacgaa 360
gcacttccat ttgctacaac tcaccttgaa tcgatc 396

<210> 23
<211> 396
<212> DNA
<213> Eucalyptus grandis

<400> 23
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gcgggttatc accccagcgt atggggggat tatttcctta aatatgattc tccctccaac 180
tcagtgaagt tcaaattcct cggaagagtg gagggacaaa ttgaggaact aaaaggagag 240
gtgaagaaga tgctgactga tatcatggat aagcccttac aaaagcttca cttgatcgat 300
caaatccaac gcttgggaat tgagtaccat tttgaacgtg aaatagatga gcaattagaa 360
caaatccaca aaagttactc tcgacttgat catgaa 396

<210> 24
<211> 700
<212> DNA
<213> Pinus radiata

<400> 24
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cggtttgatt agaaggacgg ccaatcctca tcctaatgtc tggggctatg agtttgtgaa 180
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tcctttttctg ttgagagaag ctcaatcttt ccaacttgaa ctcccttatg acctgcctta 660
tatacacaag ttgcagatga aacggcaaga gagattagca 700

<210> 25
<211> 1513

<212> DNA
<213> Pinus radiata

<400> 25
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agcgcttccg ccaatgatac agagttgcag ataagaagcg tttttaattt atttcgagct 180
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tggagatggt ggaaagaatg gggttgccca gaactaacct tcgttcgaca tcgttacgtg 540
gaattctaca ctttggtctc tggcactgac atggtgcctg aacatgctgc attcagactg 600
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ttggaggatt atatcggtag ttatcttaaa gaagcagagt ggatcgccac gggttatgtg 900
ccaacgtttc aggagtactt cgagaacggg aaactcagtt ctggtcatcg catagcgacg 960
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tgttacaagg cggacagtgc tcgtggagaa gaagcttcgt gtatatcgtg ctatatgaaa 1140
gaaaatcccg ggtcaacaca ggaagatgct ctccatcata tcaacggtat gatcgaagac 1200
atgatcaaaa aattaaattg ggagtttctt aaaccggaca acaatgctcc aatatcttcc 1260
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tacagtgttg ccagcaacga aactaaagat ctggtgatca aaaccgttct tgaacctgtg 1380
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tgcaaaggtg ttt 1513

<210> 26
<211> 295
<212> DNA
<213> Pinus radiata

<400> 26
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ttcgaaattg gagttcaata tcttccactc tgtacaacag aaagagctac aatgtctctc 120
gagatggtgg aaagaatcgg gttcccctga gctaaccttc gctcgacatc gttacgtgga 180
attctacact ttggtctgtg gcattgacat ggagcctaaa gatgccgcat tcagactgag 240
ctttgtcaaa atgtgtcatc ttatcacgat tttggatgat atttacgaca ccttc 295

<210> 27
<211> 191
<212> DNA
<213> Pinus radiata

<400> 27
acggagtgcc tacctgaata tatgaaagga gtgtacatgg tgctttacga aaccgtaaat 60
gaaatggcga aagaagcaca gaaatcacaa ggccgagaca cgctcggcta tgttcgacag 120
gctgtaataa caattgatat gctatgcata tatttgaata aacaaatact cgttggccat 180
ctattttatt t 191

<210> 28
<211> 373
<212> DNA
<213> Pinus radiata

<400> 28
ggccgacctc cttgacgaat gcggtccact gcttaagaaa gcacacgcgt ttttagaaaa 60

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gggtgcctgg actttatcta caagagatca tggttgggtt gtggctgact gctctgctga     180
agggttaaag gctgccctag aattgtcaca actgcctgaa aacattgttg gaaaaccact     240
accccagcaa aggcttttcg cttgtgtcaa ttatctactt tccatgcaga atacagacgg     300
cggttatgca acttatgact tgacacgatc ctataattgg ctagggactt tcaatcctgc     360
agcgatactt gga                                                        373
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<210> 29
<211> 1411
<212> DNA
<213> Eucalyptus grandis

<400> 29

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accagatgga cacggacaac aaactcttca atgtgggcgt cttgctcgtg gccactctcg     180
ttgtggccaa gctaatctcg gcgttgctga ttccgagatc cggaaagcgc ctccctcccg     240
tcgttaggac atggccggtg gttggtgggc tgctccggtt cttgaagggt ccgatggtga     300
tgctgcggga agagtacccc aagcttggga gcgtattcac tctgaatctg ttgaacaaga     360
aaataacgtt cttcatcggc cctgaggttt ctgcgcactt cttcaaggct tccgagtccg     420
atttgagcca gcaagaagtg taccaattca atgtgccgac tttcggacct ggagttgtat     480
tcgacgtcga ttacaccatc aggcaagagc agtttcggtt ttttactgag gctctgagga     540
ttaataagct caaggggtat gtcaatcaga tggttatgga agcggaggac tacttctcaa     600
aatggggaga tagtggcgag gtggacctaa agtatgagct tgagcacttg accatattga     660
cagcgagcag atgtcttttg ggtcgagagg ttcgtgagaa gctctttgat gatgtgtcag     720
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agaagcatgg gaacaatgtt gatcatgatg ttctttctga aatggatgtc ctgtatcggt    1140
ccatcaagga agcactgaga cttcacccac ctctaattat gctgctccga agctcgcata    1200
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ccatcaacct attcaagatt tacctatggg t                                   1411
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<210> 30
<211> 689
<212> DNA
<213> Eucalyptus grandis

<400> 30

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gcgcaccgga gggtccctct ctctctctct tcactgtcct cctccgtttt cttgctggtg      60
tcctgagggt gagaggaagt tccggctcga tctgtcggaa ccctagtcct tatccactcg     120
ccaaaaaagt tgtaaagggg acgcaaaaag agcgaggatg tggaagctca agattggaga     180
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gttcgacccg gaggccggga cccccgagga gagggccgag gtcgaggccg cccgccagaa     300
cttctacaac aaccgcttca aggtccgccc cagctccgac ctcttctggc gcttccagtt     360
cctgagggag aagaacttca agcagacgat ccctccggtc aagatcgagg atggcgagga     420
tatcacctat gagaaggcga ccgcggccgt gaagcggtgc gtcagcttct ggtctactct     480
gcagtccagc catggccact ggcctgccga gaacgccggc cccattgcgt tctacttccc     540
tcccctggtc atgagtctct acgtgactgg acatctgaac aacgttttcc atgccgagca     600
tcgcagggag atcctccgct acatttacta ccatcagaac gaagacggtg gctggggact     660
gcacattgaa ggccacagca cgatgatcg                                       689
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<210> 31
<211> 393
<212> DNA
<213> Pinus radiata

<400> 31
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ccaaggcaat ggagaacgaa gatggagtgt caggagcagt aaaggcattt cataaacatt 180
tacccaaaaa aatgccacaa ccactgccac cacctacaga tcatagtcta attgattcct 240
tctttacagg tgttggaaag gtttttggtt gtggctgatt gtaccttaat ataacgttta 300
tcaactatta ggctggtatg ctttgaaggt aaaaactgaa aatcgagtgc ttgaacttgt 360
acatatgaca aattcagatt ttgtttcctt ttg 393

<210> 32
<211> 519
<212> DNA
<213> Pinus radiata

<400> 32
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tagcaaggtt ttgaagacca ccgttccagc tttgttagaa ttgaacatgc tcaagaattt 120
gactggatct gcactggctg gtgccatggg aggattcaat gcccatgcat ccaatatcgt 180
ctcagctgta tttattgcaa caggtcaaga tcctgcccag aacattgaga gctctcattg 240
tattacgatg atggaggcat ccaacgatgg aaaggatctt catgtatcag tcaccatgcc 300
ttgtattgag gttggaacag taggaggtgg aacgcagttg gcctcacaag ctgcttgctt 360
gaatatgctc ggagtgaaag gagcgaataa ggaatccccc ggagcgaatg ctcagacttt 420
ggccagaatt gtggcaggag cagttttggc tggagagctg tctctcatgt ctgccttagc 480
tgcagggcag ctggtgaata gccatatgaa attcaacag 519

<210> 33
<211> 302
<212> DNA
<213> Pinus radiata

<400> 33
atgcttgcgt tgccaaaaac cgatgtaatt tattattgtg cgcaggaatt ccttctgctc 60
cttatgatcc cctaacccct aaatcgtagc agtgaagcca ttaacgattt ttgcgggttc 120
agaaagattc actgaatcgc ttactaaaac tctgtttcag gaatggcaac aggaggagga 180
gcgttggatc tggcctcagg aatgggaggc aacattgaga aagaacaaat gctgaccgct 240
gttgaagagt acgaaaaata tcacatgtac tatggtggtg atgaaggctc gagaaaatct 300
aa 302

<210> 34
<211> 508
<212> DNA
<213> Eucalyptus grandis

<400> 34
cttcttgcct gtctctgcct ctctctctct cgttcctagg gttctgaagc tgatcctcct 60
cctgcattgt cctcattctg ggcggggtgg ccacaatgtc gaaagcagga gcgatggatc 120
tggcgacggg ccttggcggg aagatggaca agagcgacgt cctgtccgcc gttgacaagt 180
atgagaagta tcatgtctgc tatggaggtg atgaggaaga aaggagagct aactatagtg 240
acatggtgaa taaatattat gatcttgcta ccagctttta tgagttcggc tggggagaat 300
ctttccattt tgcccacaga tggaaagggg agtctctacg agagagcatt aagagacatg 360
aacactttct tgcattacag ctaggcttaa aacctgggca caaggtgctg gatgtcgggt 420
gcggaattgg tggaccgctt agggaaatag ctcgattcag ctccgcatct gttacaggat 480
taaacaacaa tgagtaccag ataacaag 508

<210> 35
<211> 353
<212> DNA
<213> Pinus radiata

<400> 35

gttcagaata tggtttgatg ttcctgtcgt tcttcctcca ttgacacaat gctttgctga 60
cagaataagc ttggtctatg atccccacac agatgaatac tacaatgccc ctggggtgga 120
gactagagtg ccttattttg gttcaacaga aggaatgaag taccttgatc cctgcttcaa 180
gtatataacg ccatacatgt catccttggt gaaatctctt gaggatgttg gatatgttga 240
cggtaaatcc ctttttggtg caccctatga tttccgttac ggtcctggaa caaagtcctc 300
ttctgtgggg gcaaagtatt tggaaaatct gagaaaattg gtggaggagg cgt 353

<210> 36
<211> 82
<212> DNA
<213> Eucalyptus grandis

<400> 36
ggctattgga acacaatgga tattgcacac gatcgagctg gcttctacat ctgttgggga 60
tgcttggtat gggtcccatc ca 82

<210> 37
<211> 474
<212> DNA
<213> Pinus radiata

<400> 37
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agaacaggcc tgccgttgcc ttccctgtgg gaaattttg cgcagcttgc agtttatttc 120
atggttgaag actatggcaa ctattggata cacaggtggc tacattgcaa atggggctat 180
gagaagatcc atcatgttca ccatgagttc actgctccaa tgggttttgc tgctccatat 240
gcacattggt cagaggtgtt gatattgggg atccctacgt ttgtcggacc ggcaattgct 300
ccaggacaca tgattacatt ctggtgctgg gttgtgctgc gccaagtgga agcgattgaa 360
actcacagcg gatatgactt tccgtggact cttaccaaat taattccttt ctatggaggc 420
gcggagtatc atgactacca tcattatgta ggaggacaaa gtcaaagcaa cttt 474

<210> 38
<211> 340
<212> DNA
<213> Eucalyptus grandis

<400> 38
gccatcattg tgggagattc tggcgcagct cctggtctat ttcttgattg aagactacac 60
caactactgg ttgcacagat tattgcactg caaatggggg tatgaaaaga tccacagcgt 120
tcaccacgag tacagcgctc cgatcggttt tgcggcgcca tacgcgcact gggctgaggt 180
tctaatcctg ggattccttt cttttcttgg gcctgcgatt gttcctgggc acatgatcac 240
gttgtggttg tggattgctt tgcggcagat tgaggccatc gactactcac agcgggtacg 300
aattgccttg gagtcttacg aagtacattc cattctatgg 340

<210> 39
<211> 487
<212> DNA
<213> Eucalyptus grandis

<400> 39
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attgaggtga cagtcgctga tgcaagattc tgcaaaccgc ttgacatagg attacttagg 120
gagttgtgtg aaaatcatgc ctttctggtc actgttgagg aaggatccat cggaggtttc 180
gggtcccatg ttgcacagtt cattgcactt gatggacggc ttgatgggag aataaagtgg 240
cggccgattg ttttacctga tgcctatgta gagcacacgt caccaaatga gcagctttcc 300
cttgctgggc tcaccgggca tcacattgcc gcaactgtgt tgagtctcct tggccggaca 360
cgcgaagctc ttctgttgat gtgctaggtt ccctgcaatt cttccgcccc gattcctatc 420
gaaatgggct cgtgctgatg ccgcagtact gataagccag acatgttaat gaagcttgag 480
caaagat 487

<210> 40

<211> 571
<212> DNA
<213> Pinus radiata

<400> 40
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ctccagattt actgcaatct gccagtaaga gtccgttgtg gcggaagaga gctgccgaga 120
gctgccgagc tggagagcac cattcgcacc atatagagaa gggggttgat agattcctgg 180
tcaaggaaaa ctgacaataa ggtgaaaaaa acaataatta ccttcagatt atctgatcat 240
cacatggctg tagttgtgtc agctcctggt aaggttttaa taacaggagc ttatctaatt 300
cttgagaagc caaatccagg acttgtgctt accaccacag ctcgcttcta cgccattgtg 360
aagccactgc ggactagcac agattccagt agttgggcat ggctatggac agatgtgaaa 420
ttaacatcgc ctcagcttgc aaaggaggcc atctacaagc tatctctgaa gactcttagc 480
ctgcaaaatg ttgcttcttc aagtagcaat ggtaatcctt ttgtggaaca agcagtgcaa 540
tttgctgttg cagctgcaaa agaagccttt g 571

<210> 41
<211> 512
<212> DNA
<213> Eucalyptus grandis

<400> 41
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cactttcccg agaaaataat ccccccgatc tccccccggg aattcccccc cggccgttcg 120
attccggcgc gcgctccggc gatcgctcgc tcgctcgcta gccggttctt ctctcgctcg 180
ttccaccgga gatggcgggc gaatggatac tgacgttgac cgcgcagacg ccgacgaaca 240
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ccgccttcga gcaggaccgc atgtggctca atggcaagga gatatctctt tctggagata 420
gatttcagag ttgtttgaga gaaattcgag cccgtgctac tgacgttgag aataaggaaa 480
aaggaattaa aatttcaaag aaagattggg ag 512

<210> 42
<211> 445
<212> DNA
<213> Pinus radiata

<400> 42
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cggtgctata ccccggaagc ccaaatctgc tcatcccgca ctcactggga gcagaacttg 180
cttctcccgg aacccaattg ttagaaattt gattggatcc gcttctaaga tgggcgcgac 240
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tttggtggat gaagaggatc atgtcattgg gcatgactca aaatacaatt gtcacttgat 360
ggagaaaata gagtcagaga atctattgca tagagctttc agtgtgtttc tattcaatac 420
aaaatatgaa ttgcttcttc agcaa 445

<210> 43
<211> 412
<212> DNA
<213> Eucalyptus grandis

<400> 43
cctctactcc tcctcctcct cctccgctat ccttcccctc tccctcctcg tccctctctc 60
tctctctgtc gatcgaccgc catggccgac ggtgccgacg ccggcatgga cgccgtccag 120
cggcgcctca tgttcgagga cgaatgcatc ttggtggatg agaacgacaa tgtcgtcggt 180
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agggcattca gtgtgttttt gttcaactca aagtatgagc tactgcttca gcaacgctct 300
gccacaaagg taacattccc ccttgtgtgg acaaacacct gctgcagcca tccattgtac 360
cgggagtccg agctcattgc tgagaacgcc cttggggcga ggaatgctgc ac 412

<210> 44
<211> 834
<212> DNA
<213> Pinus radiata

<400> 44
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ctattttcaa gtacaggatg attatcttga ttgctttggt gatccagaag tgattgggaa 120
gattggaacc gacatcgaag acttcaagtg ctcttggttg gtggtgcaag cgcttgaacg 180
ggccaacgag agccaacttc aacgattata tgccaattat gggaagacag atccctcttg 240
tgttgcagaa gttaaggctg tatataggga tcttggaatt caggatgttt tttttgaata 300
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gcagcttgtg ctgaagtctt tcctagggaa gatatacaag cgacagaagt aacattgcag 420
atctgcaagg tgtgccgcag aatgttttaa acaagtgacc tcagaaattc ccttcttgat 480
agcagtcaca tttgatatct acgctgtaaa gtgttttaaa tgagagatct cagaaattcc 540
cttgatgata gcagtcacat ttgatttcta tgtccgtgtc taggatagtg acatggtaat 600
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ggttacagca tagtcatatc tgaagtcgta ctgtaggaaa gtgttcacaa cagatggcac 780
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<210> 45
<211> 389
<212> DNA
<213> Pinus radiata

<400> 45
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tgcgctttga tcgttcgaga tgggggaatc tgaggagagt ttgggtgcag gttcgaatct 180
caagtcagct gctgtgttgg agcaggcaaa gaaacacctt gccacagacg ctgcccaaga 240
cctcaagaag aagatcggcc ttgtctatca gctcaacatt tcacccaaga aaattggaat 300
agctgaggag gtgttcgttg tggacctcaa gaatggcaaa gtcactaaag gaccatatga 360
aggaaagcca gatgcaacat tttcctttg 389

<210> 46
<211> 469
<212> DNA
<213> Pinus radiata

<400> 46
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tttcctccag gtttcatgtt tgggatagca acttctgctt atcagtgtga aggagctgcc 120
aacgaaggtg gaaaaggccc aagcatctgg gactcatttt cacgaacacc aggcaaaatt 180
cttgatggaa gcaacggtga tgtagcagtg gatcagtatc atcgttataa ggaagatgta 240
aaactgatga aagatatggg agtggatacc tacagattct cgctttcatg gcctcgtata 300
tttccaaagg gaaaaggaga gatcaatgag gaaggagtag cctattacaa taacctcatc 360
aatgaactcc tccagaatgg aatccaagcg tctgtcactt tgtttcactg ggatactccc 420
cagtctctgg aggatgaata tggcggattt ctgaggccaa ccattgtga 469

<210> 47
<211> 349
<212> DNA
<213> Pinus radiata

<400> 47
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ggggtttcaa atttggtgca gggtcatctg cttatcaggc ggaaggagct gctcatgagg 180
gtggcaaagg cccaagcatt tgggatacat tctcccacac tccaggtaaa atcgctgatg 240
ggaagaatgg ggatgttgca gtagatcaat accaccgtta taaggaagat gtgcagcttc 300

tcaaatacat gggaatggac gtctatcgtt tctctatctc ctggtcacg 349

<210> 48
<211> 385
<212> DNA
<213> Pinus radiata

<400> 48
cgcaacgcct agtatccatg gcgctcactg tcgaagctcc tgctgctctc catctgcaag 60
aggaagaaag cgaaaatgtc aaagaaatta gcagagataa atttccggag agttttgaat 120
tcggagttgc gacctccgcc tatcaagttg aaggtgctgc aaaaggagga ggaagaggcc 180
ctagtatttg ggatacattt tcatatacac cagggaaaat tattgatgga agaaatggtg 240
atgttgcagt ggatcaatac catcggtaca aggaggatgt ggatttaata gcaaaaatgg 300
gattcaatgt gtatcgtttc tcaatatctt ggtctcgaat ctttccagat ggatttggag 360
ctgaagtgaa taaggaagga atagc 385

<210> 49
<211> 417
<212> DNA
<213> Pinus radiata

<220>
<221> unsure
<222> (209)...(212)

<400> 49
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tcatgtttgg ggtagcaact tctgcttatc agtgtgaagg agctgcaaaa gaaggtggaa 180
gaggtccaag catctgggac tcatttttnn nncagacacc aggcaaaatt gttgatggga 240
gcaacggtga tgtagctgtg gaccagtacc atcgttataa ggaagatgta aaacttataa 300
aagatatggg agtggatgtc tacagattct caatctcatg gtctcgaatg tttccaaaag 360
gaaaagggga gatcaatgag gaaggagtag cctattacaa taacctcata aatgaac 417

<210> 50
<211> 264
<212> DNA
<213> Pinus radiata

<400> 50
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agaagagttg cagacatgga tattaatggt cactgcaaga gctcctacaa atatagcagt 120
gatcaagtac tgggggaaaa gagatgaaaa gctgatcctt cccatcaatg acagcatcag 180
ctttactttg gatccagacc atctgtcagc cacaaccact gtagcagtta gcccatcatt 240
cacatctgat agaatgtggc tcaa 264

<210> 51
<211> 417
<212> DNA
<213> Eucalyptus grandis

<400> 51
ctgttttatt atgggaaaga gacaagtacc tcaccaagac gaagatacaa tttgtctccg 60
tttgcaatat ccctaaatga gcttacacca ggcttacaag aaaaactgcc tccaactgat 120
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gagaagttaa gactggaaca catacagaga caggcaagaa agttacagga gggaggttgg 240
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gaagctcgag aagcatacga actgggatgg aatccctgac atattcgggc aaaaatgttg 360
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<210> 52

<211> 305
<212> DNA
<213> Pinus radiata

<400> 52
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aactctgtgg atatttaccc acttggaagg acacgtgtgg tgctaaagaa atccggagac 240
gttctagatt tggtgccgcc tccatctaaa gttcataacc taatttttgg acgaacttgg 300
attga 305

<210> 53
<211> 474
<212> DNA
<213> Eucalyptus grandis

<400> 53
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atggagcaga tgaagcagca cctctccacc gacgccggca aggcggtcac caagaagatc 180
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<210> 54
<211> 562
<212> DNA
<213> Pinus radiata

<400> 54
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caggatttct tcttgtccaa acaggtttaa ggaaatggca ggcacaagtg ttgctgcagc 180
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<210> 55
<211> 1961
<212> DNA
<213> Pinus radiata

<400> 55
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tcattcgtat tgctttgaga gagtagcgga attcgcagac agaccctgtc tgatcgatgg 240
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caatcctttc tacaagccgg gcgagatcgc caaacaggcc aaggccgcgg gcgcgcgcga 480
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caacgcccta cactcttgcg atcgctttca atatgcatat tactataaac gatatatgtt 1920
tttttataa atttactgca cttctcgttc aaaaaaaaa a 1961

<210> 56
<211> 414
<212> DNA
<213> Eucalyptus grandis

<400> 56
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accccaccca catacagaca agtagatacg cgcacacaga agaagaaaag atgggggttt 180
caatgcagtc aatcgcacta gcgacggttc tggccgtcct aacgacatgg gcgtggaggg 240
cggtgaactg ggtgtggctg aggccgaaga ggctcgagag gcttctgaga cagcaaggtc 300
tctccggcaa gtcctacacc ttcctggtcg gcgacctcaa ggagaacctg cggatgctca 360
aggaagccaa gtccaagccc atcgccgtct ccgatgacat caagcctcgt ctct 414

<210> 57
<211> 469
<212> DNA
<213> Eucalyptus grandis

<400> 57
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cttctccgaa caaacccaaa ggtactgcct tacccccgga gctgccgggc gcatggccga 180
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gccccaaatc caaggcggga atccacttgg gctacgggta tgccggtttt ggcttcgtag 420
aatacgggga cttttggcgc gagatgagga agatcaccat gctcgagct 469

<210> 58
<211> 760
<212> DNA
<213> Eucalyptus grandis

<400> 58
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tattggagac cagcgtctac ccaagagagc cagagcccat gaaggagctc agggaaataa 240
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taagggtagt ttctcatttc atcaatgctt gattttgaga tctcctttct ggtgcgatca 720
gctgacccgg cggcacaggt gatgccatcc ccgacgggaa 760

<210> 59
<211> 468
<212> DNA
<213> Eucalyptus grandis

<400> 59
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aactatatgg tcagccccat caacgatctt gtatcgagcc tggctcgaa cccgagcgtc 420
cctccggtga cttgcatcaa tctcggatgg tttcatgaca ctcgtgac 468

<210> 60
<211> 684
<212> DNA
<213> Pinus radiata

<400> 60
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gctctgcgaa catcgccaca gtggttgggg cctccgatcg aagtcatccg cgctgctact 540
cactccatcg agcgggagat caattccgtc aacgacaatc cgttaatcga tgtctccagg 600
gacatggctc tccacggcgg caacttccag ggaacaccca tcggagtttc catggacaac 660
atgcgaatct ctttggcagc cgtc 684

<210> 61
<211> 479
<212> DNA
<213> Pinus radiata

<400> 61
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ttaaaagcac tgggctgtgc acggacttcg gctcgtctgg cagcgatcca ctgaactggg 180
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gggtcgagga gagttcaaac tgggttctca cccagatgac caaggggacg gatacctatg 420
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<210> 62

<211> 1785
<212> DNA
<213> Pinus radiata

<400> 62
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ggggaatttt actgctaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1785

<210> 63
<211> 475
<212> DNA
<213> Pinus radiata

<400> 63
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<210> 64
<211> 957
<212> DNA
<213> Pinus radiata

<400> 64
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<210> 65
<211> 471
<212> DNA
<213> Pinus radiata

<400> 65

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acagacatac ttctcactgc caatcaggct acaggtagat actacatggc tgctcgagca     120
tattccaacg ggcaaggagt tcccttcgat aacaccacta ccactgccat tttagaatac     180
gagggaagct ctaagacttc aactccagtc atgcctaatc ttccattcta taacgacacc     240
aacagtgcta ctagcttcgc taatggtctt agaagcttgg gctcacacga ccacccagtc     300
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tgtccggggc agtcttgtgg aggtccaacg gatcaagatt tgcagcaagt atgaatacat     420
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<210> 66
<211> 1010
<212> DNA
<213> Pinus radiata

<400> 66

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ttgcagcatt aagcaaagaa gatgagttca tttttcacag ccctttttcct gcagtacctg    120
ttccagagaa tataagtctt ttccagtttg ttctggaagg tgctgagaaa taccgtgata     180
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<210> 67
<211> 1410
<212> DNA
<213> Pinus radiata

<400> 67

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atgaattact atggggactc ttgccctcag gctgaagaga tcattgctga acaagtacgc     180
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attctagtat aattttgtca tcagttaaag ttgctcatct gataataact ggaaacggta 1320
aaatatgaca actacgtatc ttctttggtc atctgataat aaccggaaac gataaaatat 1380
gacaactaca tatattcttt aaaaaaaaaa 1410

<210> 68
<211> 607
<212> DNA
<213> Eucalyptus grandis

<400> 68
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acttaggtca actgcaacat ttcttgatca caacatatta caatattcct aagcagagag 180
agagagagag agagagagag agagagagag agagtttgaa tcaatggcca ccgccggaga 240
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tgatgctctt taccaatata ttttggagac cagcgtgtac ccaagagagc ctgagcccat 360
gaaggagctc agggaaataa cagcaaaaca tccatggaac ataatgacaa catcagcaga 420
cgaagggcag ttcttgaaca tgcttctcaa gctcatcaaa gccaagaaca ccatggagat 480
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gattttggct atggacatta acagagagag ctatgaactt ggcctgccgg catccaaaaa 600
gccggtg 607

<210> 69
<211> 421
<212> DNA
<213> Eucalyptus grandis

<400> 69
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ccaagtctcg gacgaggagg cgaacctctt cgccatgcag ctggcgagcg cctccgtgct 180
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gccgggcgcg ttcctctccc cgggggaagt cgcggcccag ctcccgaccc agaaccccga 300
ggcacccgta atgctcgacc ggatcttccg gctgctggcc agctactccg tgctcacgtg 360
caccctccgc gacctccccg atggcaaggt cgagcggctc tacggcttag cgccggtgtg 420
c 421

<210> 70
<211> 508
<212> DNA
<213> Eucalyptus grandis

<400> 70

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atatcgtgaa aggagtccgt cgacgacaat ggccgagaag agcaaggtcc tgatcatcgg 180
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cttcaagaac ttgggcgtca ctctgctcat cggtgatctg tacgatcatg agagcttggt 360
gaaggcaatc aagcaagccg acgtggtgat atcgacagtg gggcacatgc aaatggcgga 420
tcagaccaaa gaatcgtcga cgccattaaa ggaagctggc aacgttaagg tttgttggtt 480
ggttcatttg atctggtttg ggggggtc 508

<210> 71
<211> 495
<212> DNA
<213> Eucalyptus grandis

<400> 71
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aagaggaagg tggggcagcc taaaggggca ctgcgggtca ctgcatcaag caataagaag 180
atcctcatca tgggaggcac ccgtttcatc ggtgtgtttt tgtcgagact acttgtcaaa 240
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agaaaggatt ttgattttgt taaatctagt cttgctgcag aaggctttga cgttgtttat 420
gacattaacg gcgagaggcg gatgaagtcg caccaatttt ggatgcctgc caaaccttga 480
accagtcaac tactg 495

<210> 72
<211> 472
<212> DNA
<213> Eucalyptus grandis

<400> 72
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cctcgtcgtt ggcggcactg gctacctcgg gcggaggttc gtgagggcga gcctggacca 120
gggccacccc acgtacgtcc tccagcgtcc ggagaccggc ctcgacattg agaagctcca 180
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ccacttccgg agccacaaca tcctgatgca gctcaagctc gtggaggcta tcaaagaagc 360
tggaaatgtc aagcggtttt tgccgtcaga gttcggaatg gacccggccc tcatgggtca 420
tgcaattgag ccgggaaggg tcacgttcga tgagaaatgg aggtgagaaa ag 472

<210> 73
<211> 380
<212> DNA
<213> Eucalyptus grandis

<400> 73
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tcgagagctt gtcgagcagt ggcattcagt cgatcccgca ggagtatgtg aggccgaagg 120
aggagctcac aagcattggc gacatcttcg aggaggagaa gaagcatgag ggccctcagg 180
tcccgaccat cgacctcgag gacatagcgt ctaaagaccc cgtggtgagg gagaggtgcc 240
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tccccaacga cctgattgag cgtgtaaaga aggctggcga ggtgttcttc aacctcccga 360
tcgaggagaa ggacaagcat 380

<210> 74
<211> 515
<212> DNA
<213> Eucalyptus grandis

<400> 74

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ctctctctct ctctctctct gtgtgttcat tctcgttgag ctcgtggtcg cctcccgcca      60
tggatccgca caagtaccgt ccatccagtg ctttcaacac ttctttctgg actacgaact     120
ctggtgctcc tgtctggaac aataactctt cgttgactgt tggaagcaga ggtccaattc     180
ttcttgagga ttatcacctc gtggagaaac ttgccaactt tgatagggag aggattccag     240
agcgtgtggt gcatgccaga ggagccagtg caaagggatt ctttgaggtc actcatgaca     300
tttcccagct tacctgtgct gatttccttc gggcaccagg agttcaaaca cccgtgattg     360
tccgtttctc cactgtcatc cacgaaaggg gcagccctga aaccctgagg gaccctcgag     420
gttttgctgt gaagttctac acaagagagg gtaactttga tctggtggga aacaatttcc     480
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```

<210> 75
<211> 487
<212> DNA
<213> Eucalyptus grandis

<400> 75

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gaattcggca cgagctccca cttctgtctc gccaccatta ctagcttcaa agcccagatc      60
tcagtttcgt gctctcttcg tcatctctgc ctcttgccat ggatccgtac aagtatcgcc     120
cgtccagcgc ttacgattcc agcttttgga caaccaacta cggtgctccc gtctggaaca     180
atgactcatc gctgactgtt ggaactagag gtccgattct cctggaggac taccatctga     240
ttgagaaact tgccaacttc gagagagaga ggattcctga gcgggtggtc catgcacggg     300
gagccagcgc gaaagggttc ttcgaggtca cccacgacat ctctcacttg acctgtgctg     360
atttcctccg ggctcctgga gtccagacgc ccgtaatcgt ccgtttctcc accgtcatcc     420
acgagcgcgg cagcccgaac ctcagggacc ctcgtggttt tgcagtgaag ttctacacca     480
gagaggg                                                               487
```

<210> 76
<211> 1474
<212> DNA
<213> Pinus radiata

<400> 76

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gaattcggca cgagaaaacg tccatagctt ccttgccaac tgcaagcaat acagtacaag      60
agccagacga tcgaatcctg tgaagtggtt ctgaagtgat gggaagcttg gaatctgaaa     120
aaactgttac aggatatgca gctcgggact ccagtggcca cttgtcccct tacacttaca     180
atctcagaaa gaaaggacct gaggatgtaa ttgtaaaggt catttactgc ggaatctgcc     240
actctgattt agttcaaatg cgtaatgaaa tggacatgtc tcattaccca atggtccctg     300
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gagagcatgt aggggttggt tgcattgttg ggtcctgtcg cagttgcggt aattgcaatc     420
agagcatgga acaatactgc agcaagagga tttggaccta caatgatgtg aaccatgacg     480
gcacacctac tcagggcgga tttgcaagca gtatggtggt tgatcagatg tttgtggttc     540
gaatcccgga gaatcttcct ctggaacaag cggcccctct gttatgtgca ggggttacag     600
ttttcagccc aatgaagcat ttcgccatga cagagcccgg gaagaaatgt gggattttgg     660
gtttaggagg cgtggggcac atgggtgtca agattgccaa agcctttgga ctccacgtga     720
cggttatcag ttcgtctgat aaaaagaaag aagaagccat ggaagtcctc ggcgccgatg     780
cttatcttgt tagcaaggat actgaaaaga tgatggaagc agcagagagc ctagattaca     840
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ttcagatgtt tttttaactt gtatatgtaa agatcaattt ctcgtgacag taaataataa    1380
tccaatgtct tctgccaaat taatatatgt attcgtattt ttatatgaaa aaaaaaaaaa    1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                                1474
```

<210> 77
<211> 414
<212> DNA

<213> Eucalyptus grandis

<400> 77

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cacgctcgac gaattcggta ccccgggttc gaaatcgata agcttggatc caaagcaaca    60
cattgaactc tctctctctc tctctctctc tctctctctc tcccccaccc cccccttccca   120
accccaccca catacagaca agtagatacg cgcacacaga agaagaaaag atgggggttt   180
caatgcagtc aatcgcacta gcgacggttc tggccgtcct aacgacatgg gcgtggaggg   240
cggtgaactg ggtgtggctg aggccgaaga ggctcgagag gcttctgaga cagcaaggtc   300
tctccggcaa gtcctacacc ttcctggtcg gcgacctcaa ggagaacctg cggatgctca   360
aggaagccaa gtccaagccc atcgccgtct ccgatgacat caagcctcgt ctct          414
```

<210> 78
<211> 273
<212> DNA
<213> Eucalyptus grandis

<400> 78

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ctttgatgat gtgtcagccc tcttccacga ccttgacaat ggaatgctac cgatcagtgt    60
catcttcccc tacctgccca tcccagctca ccatcgtcgc gataaggctc ggaagaagct   120
ttctgagatt tttgcaaaca tcatttcttc acgaaaatgt gctggcaaat cagaagaaga   180
catgttgcag tgcttcattg actccaagta caaaaatggt cgcccgacaa ctgaggccga   240
ggtcactggt ctgcttattg cggctctctt tgc                                 273
```

<210> 79
<211> 121
<212> DNA
<213> Eucalyptus grandis

<400> 79

```
ctacctcctc accaacaaga agtacctctc tgccgtctct aatgaacaga agcacctgat    60
ggagaagcat gggaacaatg ttgatcatga tgttctttct gaaatggatg tcctgtatcg   120
g                                                                    121
```

<210> 80
<211> 505
<212> DNA
<213> Eucalyptus grandis

<400> 80

```
ggaggctgaa gatagcagaa ggagaggacg gtccctacct gtacagcacc aacaactacg    60
tggggagaca gatttgggag ttcgatccgg aggctggcac cgctgaggag cgcgcggagg   120
tcgaggctgc tcgccagcac ttctacgacc accgccacca agtcaagccc tgtggcgacc   180
tcctctggcg catgcagttc ctgagggaga aggagttcaa gcagacgatt ccgccagtga   240
gggtggagga tggcgaggag atcacctacg acaaggcgtc caccgcgctg aagcgggccg   300
tccatttctt ctccgccctg caggctagcg acggtcattg gcctgccgag aacgccggcc   360
ctctcttctt cctccctccc ctggtcatgt gcgtctacat caccggccac cttgacgccg   420
tcttccccgc cgagcatcgc aaagagattc tccgctacat ctacaaccac cagaatgaag   480
atggtggatg gggcttgcac atcga                                          505
```

<210> 81
<211> 270
<212> DNA
<213> Eucalyptus grandis

<400> 81

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catggatgac attgtctctc acgagtttga gcaaaagagg ggccatgtag tatctgcagt    60
ggagttgctc ataaaatatc gtggtgtctc ggagcaggaa gctgtggagg aactccagaa   120
acgagtcatt gatgcatgga aggacaccaa tgaagagttt ctccgtccaa ttgcggtccc   180
aatgccgatt ctcacgcgag tgctcaattt atcgcgggtg attgatgtgt tatatagcga   240
tggggataat tacacccatt ctgaaaccaa                                     270
```

<210> 82
<211> 441
<212> DNA
<213> Eucalyptus grandis

<400> 82
gtttcgtctc gggagagtaa agtctctctg tctctctctc tctctctctc cgagcgtccg 60
ccatggagga tgatcgagat cgggggcttc tttacgattc agatccgccg tctccatcgc 120
tctccccgcc actctccccg ccgcggccgt tcgcgctcac cttcttcgac agggagaggc 180
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atcgcgtaca caaagatgcg gttgctgact gggttttatc tttccaagct catccgagga 360
gtaaagctga tctagacaat ggacaatttt atgggtttca tggttccaga agctcacagt 420
tcccttcaaa agataatgcg a 441

<210> 83
<211> 467
<212> DNA
<213> Eucalyptus grandis

<400> 83
tttttttaga ttatattttg cgtctacaaa cgtgctcgag gcaacggtct ctgtttcgtc 60
tcgggagagt aaagtctctc tctctctctc tctctctccg agtgtcagcc atggaggatg 120
atcgagatcg gggcttctt tacgattcag atccgtcgtc tccatcgctc tccccgccgc 180
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ctgactgggt tttatctttc caagctcatc cgaggagtaa agctgatcta gacaatggac 420
aattttatgg gtttcatggt tccagaagct cacagttccc ttcaaaa 467

<210> 84
<211> 396
<212> DNA
<213> Pinus radiata

<400> 84
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ttaaaagaag ccatactaaa gcttccggtc tgcactcttt cacgagagat atcgtacgtt 120
atggaatatg gttggcatat aaatttgcca agattggaag caaggaacta catcgacgtg 180
tttggacagg accccattta tttgatgcca aatatgaaga cccaaaaact tctagaactc 240
gcaaagttgg agttcaatat gtttcactct ttacaacagc aagagctaaa acttctctcc 300
agatggtgga aagattcggg tttctctcaa atgaccttcc ctcggcatcg tcacgtggaa 360
tattacactt tggcatcttg cattgatagt gaacct 396

<210> 85
<211> 462
<212> DNA
<213> Pinus radiata

<400> 85
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ctcaatttat ttcgggcctc cctcgttgcc tttccggggg agaatgttct gggagaggct 180
gaaatattct ctacaacata tttaaaagaa gccctgaaaa cggttccgat ttccagtgcc 240
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accaagaaag agaagctttt agaactcgca aaattagagt tcaatatctt tcactccttg 420
caacagaaag agttaaagca tgtgtccaga tggtggaaag at 462

<210> 86
<211> 247

<212> DNA
<213> Pinus radiata

<400> 86
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agtctttcag gagagattga atacgttatt gaatatggtt ggctcacaaa tttcccgaga 180
ttggaagcac gaaattatat cgacgtattt ggaaaggaca ccattccctg tgttaagacg 240
acgacca 247

<210> 87
<211> 426
<212> DNA
<213> Pinus radiata

<400> 87
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gttcct 426

<210> 88
<211> 488
<212> DNA
<213> Pinus radiata

<400> 88
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cttccagaat atatgaaagg catatatatg gtgttttacg atgcgttaat caaatggctc 480
gagaggcg 488

<210> 89
<211> 223
<212> DNA
<213> Pinus radiata

<400> 89
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cacatactct gccaaataga ttatcgatcc aaatttgcat atctcatagg tttgataggg 180
cgtttgctga atgataccaa aacttaccag gcggagcgag gtc 223

<210> 90
<211> 318
<212> DNA
<213> Pinus radiata

<400> 90
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aaaatgacgg tttcacacat tcacatgaaa cggaaattaa agagcatgtc aaaaagatac 180

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aatgcccgca atgaaatt                                                   318
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<210> 91
<211> 1695
<212> DNA
<213> Eucalyptus grandis

<400> 91

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atcaagtcgg tcgtcgaggg aaagatgccg tcgtactcgc tcgagtccaa gcttggggac     180
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aggtccagca aagacgttac caaggtctcc tcttaaatta taaacacgag aaaaaaatta    1380
ccatgcgtcc cgaaaggaag gaggggccac ggaagaatcc tcgatttatg ctcgtataag    1440
gcataccgga gaatagtggg tatcgtatat agccagctct ttagatccag ggtcagatgg    1500
cgagagagag agagagagag aggaaaagaa aaggagagct tgcagagaag aaactggact    1560
cgaagagtcg agtttgtgat ctgcgttctt tctttctttc tttctttctc gtacttgttc    1620
tgttttctac tttcctgaat taaaaaggca acgtaagaat gtcctgcaaa tattgtaaat    1680
cgtccttaaa gttta                                                     1695
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<210> 92
<211> 315
<212> DNA
<213> Eucalyptus grandis

<400> 92

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tcccgaaatc gcgaagccga cgccgtcgtt cccctcgcgc tcgcttccca gtcggcatgt      60
ctgaacctgc taggggtgaa aggcgaaaag gagctagcgg gagccaactc gaggctcctg     120
gccacggtcg tgtccggcgc cgtccttgcc gccgagctct ccctcatgtc cgctatcgcg     180
gcggggcagc tcgtgaagag ccacatgaag tacaacaggt ccagcaaaga cgttaccaag     240
gtctcctctt aaattataaa cacgagaaaa aaatcacgat gcgtcccgaa aggaaggagg     300
ggccacggaa gaatc                                                      315
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<210> 93
<211> 244
<212> DNA
<213> Eucalyptus grandis

<400> 93

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acctctacct aaggttctcg tgcagcaccg gtgacgcgat ggggatgaac atgatctcaa      60
agggagtcca gaacgtcatg gatttcctgc agaaggactt ccccgacatg gacgtgatgg     120
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```
ggatctccgg aaacttctgc tcggataaga agcccgcagc tgtgaactgg attgagggga      180
ggggcaagtc ggttgtgtgc gaggccgtga tcaagggcga cgtggtgagg aaggtgctca      240
agac                                                                   244

      <210> 94
      <211> 244
      <212> DNA
      <213> Eucalyptus grandis

      <400> 94
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tgacgcgatg gggatgaaca tgatctcaaa gggagtccag aacgtcatgg atttcctgca      120
gaaggacttc cccgacatgg acgtgatggg gatctccgga aacttctgct cggataagaa      180
gcccgcagct gtgaactgga ttgaggggag gggcaagtcg gttgtgtgcg aggccgtgat      240
caag                                                                   244

      <210> 95
      <211> 419
      <212> DNA
      <213> Pinus radiata

      <400> 95
ggaaaatcag tagtttgtga agctctaata aaggaagaag tggtgaagca ggtgctgaaa       60
actaatgtgg ctgcccttgt tgaactcaac atgcttaaaa atcttactgg atcggcagtt      120
gccggtgctc ttggtggttt taatgcccat gcaagcaaca tagtctctgc aatatatata      180
gcaactggac aggatccagc tcagaatgtt gagagttctc attgcatcac catgatggaa      240
gctgttaatg agggaaggga tcttcacata tctgtcacca tgccttccat agaggttggc      300
actgttggag gtggtactca gcttgcgtct cagtctgctt gcctgaacat gcttggcgtc      360
aagggtgcaa acaaagagtt ccctggagct aatgcgaggc tcctggcgac cattgtacc       419

      <210> 96
      <211> 856
      <212> DNA
      <213> Eucalyptus grandis

      <400> 96
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ggcggcagcc gaagcccccg cgcccgcgg ccggcgaccc ccgccgccgc cagaagagcc       120
tccggctgcc ggccccgggc gtcgaccgcc gcgagccctc gccgtcgtcg cccaaggcgt      180
cggacgcgct cccgctgccg ctgtacctca cgaacgccgt cttcttcacg ctcttcctct      240
ccgtcgcgta ctacctcctc caccggtggc gcgacaagat ccgcagctcc gtcccgctcc      300
acgtcgtcac cttccccgag atcgccgcca tcgtctccct catcgcctcc ttcatctacc      360
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cgtgggacgt gctcgacgac gaggtcgccg tgggcggcga cggcttcctc ccggaggacg      480
acggccctcc ctgcgccgcc attgcgtgcg ctcctccgaa gctggccgag cgcgaaccta      540
tcgactccgc cctgtcgtcc gccgaggacg aggaggtcgt gaagtccgtc acggacggta      600
aaatcccgtc gtactcgctc gagtccatgc tcggggactg caagagagcc acttccatcc      660
ggcgcgaggc actgcagcgg atgaccggga ggtcgctgaa gggcttgccc ctcgaagggt      720
tcgactacga gtcgatcctg ggtcagtgct gcgaaatgcc ggtcgggtac gtgcagattc      780
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caccgagggt tgcttg                                                      856

      <210> 97
      <211> 863
      <212> DNA
      <213> Eucalyptus grandis

      <400> 97
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ggcggcgggc tcctccctcg acgccaaatc caagcactcg ccatcgccgc tcaagtacta      120
cgccgacgag gacccgtcgc tgaaggtccc cgccttcctt tacctggtca acgcctccgc      180
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cgcctcctcc gtctacctcc tcggcttctt cggggtcgag ttcttccagt ccctcctcct     360
ccgccccccc tccgacatct gggccgacga cggcgaggaa gagagggtgg tctccgtagt     420
tgccgaggag ggcgcgctga aagcgccctg tggccaggcc cttgatgagg agaccaccaa     480
gctggagttc gaccccgtta agcccgctgc tccgaaggcg aagccggtcg agacagagaa     540
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gatccgccgt gaggcactgc agaggaagac cgggaagtcg ctcgccggat tgccgctgga     720
agggttagac tacgactcga ttctcgggca gtgctgcgag atgccagttg ggtacgtgca     780
gatccccgtg ggaatcgcgg ggccacttgt gctcgacggg cgggagtact cggtcccgat     840
ggccacgact gaagggtgcc tgg                                             863
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<210> 98
<211> 668
<212> DNA
<213> Eucalyptus grandis

<400> 98

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cccctccgcc gcgcgcggcg gcggaagagg ccccgcttca tcgtcccctc ccctcgagcc     180
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cttcatctac ctcctcggct tcttcggcat cgacttcgtc cagaccttca tcgcgcgcgc     420
ctctcacgac gcgtgggagg acctcgacga cgatgtcaac cgcggcttcg gctgtacgga     480
catcgtggct ccgctcccga aatcgggcga tccggcgccg gtgatctcgg ctttgtcctc     540
tgccgaagac gaggagatcg tcaaatccgt cgtggacggc acgattcctt cgtattcgct     600
ggaatctaag ctcggcgact gcagaagagc ggctttcgtt cggcgtgagg ctttgcagag     660
aacgactg                                                              668
```

<210> 99
<211> 430
<212> DNA
<213> Pinus radiata

<400> 99

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cacattataa gcaagcaggg atgtctcctg tttctgtgat ctcgttgcct tccgacttct      60
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ttccaaatgt cgcgatgcac aggcaacgga aattaatgac acatgcttcc atgagcatga     180
atttgaggac cgccgtatct gatgatgctg ttataagacg cagaggtgat ttccattcca     240
acctctggga cgatgatttt atacagtccc tttcctcgcc ttatggggaa ccttcttatc     300
gggaacgtgc tgagagactg attggggaag taaagaatag gttcaattca gtgtcaaacg     360
aagatgggga atcaatcact cccctcgatg atctgattca aggcctttgg atggtcgaca     420
gtgttgaacg                                                            430
```

<210> 100
<211> 478
<212> DNA
<213> Pinus radiata

<400> 100

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gttgtcttga gccgtctatg taggcgaaaa cgtatcataa tatataagcc aacgtaaatg      60
gctctggttt ctgctgtccc gttgaattcc aaactgtgtc tgtgcagaac gttgttcggt     120
tttagtcatg agctgaaagc tatccatagt acagtcccaa atcttggaat gtgcagggga     180
gggaaatcca tagcaccttc tatgagcatg agttcgacca cctccgtttc taatgaggat     240
ggggtaccaa gacgcatagc tggtcatcat tccaaccttt gggacgatga ttccatagcc     300
tctctctcca cttcctatga ggcaccttct taccgtgagc gcgctgataa acttataggg     360
gaagtaaaaa atatcttcga tttaatgtca gtggaggatg gagtattcac cagtcccctc     420
agtgacctcc atcaccgcct ctggatggtc gatagcgttg aacggttggg aatcgata       478
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<210> 101
<211> 204
<212> DNA
<213> Pinus radiata

<400> 101
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tctgatgatg atatacaaag acgcacgggc ggttatcatt ccaacctctg gaacgacgat 120
gtgatacagt ttctgtcaac gccttatggg gaactcgctt accgtgaacg tgctgagcga 180
ctgattgatg aagtaaggaa cata 204

<210> 102
<211> 299
<212> DNA
<213> Pinus radiata

<400> 102
tgatgatgct gttataagac gcagaggtga ttaccattcc aacatctggg actatgattt 60
catacagtcc ctttccgcgc cttatgggga accttcttac cttgaacgtg cggagagact 120
gattgaggaa gtaaagaagg tattcaattc aatgtcagag gagaatggcg aattaatcac 180
tcccctgaat gatctgattc aacgcctttg gatggtcgac agtgttgaac gtttggggat 240
cgatagacat ttcgaaaatg agattgaatc agcgctggat tatgtttaca gttattgga 299

<210> 103
<211> 399
<212> DNA
<213> Pinus radiata

<400> 103
cctcggccgc gaccacgcta cctaacctgg acactattct tacatctatt ccaccagagg 60
tcatattgag gaagcagcga ttgctcgcta atcctgccat gaagcaggcc atgctgtttc 120
cacaacctgc tcaaccagga gatgcgttcc atcagatttt gaatggtcta gcccgcaaat 180
tgcctcatga tagcagtatt tacttgaaac ctaatcaaaa gattttgaac tggacagcag 240
gccctcctgc tgatctaaag ccctggtagc atatacacat tgtgtaatca aattgccaat 300
gtaccttcac ttaacacatc aagataagtt ttaaggcaat agccattcta ttctttttgta 360
gcttatcatt tataagttat gttcagacaa catataagt 399

<210> 104
<211> 672
<212> DNA
<213> Pinus radiata

<400> 104
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cacttttgct gcagggctgg cttgtgaagg cctgaagcct ttttgtgcta tatattcctc 120
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gaccgaacta tttcacatgg ttgcaaccgc agctgctatt gatgatcgcc ctagttgctt 360
cagatttcca cgaggcaatg gagtaggtgc acagctgcca cctggtaaca aaggagtgcc 420
cttagagatt gggaaaggta gaattttagt tgaaggtgat cgagtagcac tcttagggta 480
tggtactgtt gttcaaaatt gccttgctgc cagtgcttta ctggaagagc aagatttatc 540
tgtgacagtt gcagatgcca gattctgcaa gccacttgat cgtgatctaa ttcgatctct 600
tgcaagggag cacgaggtat taataacagt cgaggaggga acaataggag gttttggatc 660
acatgttgct ca 672

<210> 105
<211> 971
<212> DNA
<213> Pinus radiata

<400> 105
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atcagttaag ttcgatgggt ttcgcattct cgtctggaag tctatgccac caaatcaagc 120
ctacaaagct cgaatccatg aagttgggaa ggcgggttgg taaagcttat gccagtgctt 180
tatctgacca aggagagtac tattcagaga agccaccgac acctctcctg gatacaatca 240
attatccgat tcatatgaag aatctctcta ttcgagagct caaacaactt tcaaatgaac 300
ttcgttctga cataattttt gaggtttcaa gaaccggtgg ccaccttgga tctagccttg 360
gtgtggttga acttacggtg gcacttcatt atgtctttga tgctcctgag gataagatat 420
tatgggacgt tggccatcag gcttatcctc acaagattct tactggtaga agagataaga 480
tgcccacatt gagacagaca aatggcctct caggctttac aaaacgttca gagagtgaat 540
atgactgctt tggtgctggt cacagctcta ctagtatatc tgccgggcta ggcatggctg 600
ttggtcgtga cttgaaaggg gaaaacaatc atgtcattag tgtcattgga gatggtgcca 660
tgacagctgg gcaagccttt gaagctatga acaatgcagg atatttggat tccaacatga 720
tcgttattct gaatgacaac aaacaagttt ctctgccaac agcaaatctt gatgggccta 780
taccaccagt gggtgcactc agcagtgcac tgagtaagct tcaatcaagt aaacctttgc 840
gtgaactaag agaggttgcc aagggtgtta ccaaacaact cggtgccccc atgcatgaac 900
tggcagcaaa agtggacgag tatgcacgag gtatgatcag tggttcccgt tccacgctgt 960
ttgaggagct g 971

<210> 106
<211> 265
<212> DNA
<213> Eucalyptus grandis

<400> 106
aggcggtcat ctgagcgcga gcctcggcgt ggtggaactc acggtcgctc ttcacaatgt 60
tttcaatgcc ccagaagaca aaatcgtatg ggacgtggga catcagacat acccccacaa 120
gattctgacc ggacggcgga ctcggatgca cacgattagg aagacctcgg ggcttgcggg 180
gtttcccaag agggatgaga gcgtttatga tacatttggc gtgggacaca gttctacgag 240
catctccgcc ggtctcggta tggcg 265

<210> 107
<211> 295
<212> DNA
<213> Eucalyptus grandis

<400> 107
cccctgtccg ggaaaagctt gtcaaagcat ggagaaatga ctctgagatc tttgctcact 60
atggccggct caccacgcca tactctgatg agcttctcgg gagcaaattt tgcctccatg 120
tcaaaggctt tgaagtaaac acagcccgca ttgcagattc attgtattat ggctgtgtcc 180
ctgtgataat cgccaatcac tatgatctcc cattcgcgga catattgaac tggaagagct 240
tctcggtcgt ggttgccact ttggacattc cattgcttaa gagaatcctc aaggg 295

<210> 108
<211> 456
<212> DNA
<213> Eucalyptus grandis

<400> 108
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ctttttgatg ctatagttag cttgtgcatc ccagttatcg tcagtgacag tatcgagttg 120
ccatttgaag atgtcataga ctaccggaaa attgcaatat ttgtagatac tgccacttct 180
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cgtgacaaga ggattgtcaa gagggacatg agtgaaccag actgttcctg tatctgttcg 420
aaccagacgg gggtcatttc cactctatga cacgag 456

<210> 109
<211> 640

<212> DNA
<213> Eucalyptus grandis

<400> 109
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ccgcgggtta tcaccccagc gtatgggggg actacttcct taaatatgat tctccctcca     180
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tctttgacaa attcaaagat agcaacggga acttccgaga gtcgctcata agtgatgtgc     540
ggggattgct gagcctatat gaagcttgcc atttaaggtg tcatggcgat tcaatcttgg     600
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```

<210> 110
<211> 396
<212> DNA
<213> Eucalyptus grandis

<400> 110
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tcagcaactc catgcgctcc ttcgaataaa ggaacaggcc atgtgatcga acgccggtcg     120
gcgggttatc accccagcgt atggggggat tatttcctta aatatgattc tccctccaac     180
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caaatccaac gcttgggaat tgagtaccat tttgaacgtg aaatagatga gcaattagaa     360
caaatccaca aaagttactc tcgacttgat catgaa                               396
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<210> 111
<211> 348
<212> DNA
<213> Eucalyptus grandis

<400> 111
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gttcttcagc tacctagatc tagaaagtag caaaaaaaga aatgtctctt ccgatttcaa      60
gagtcccatc ttcttctcct gctgaaaaaa caagcctggt ccctgaaggc ggatcggcaa     120
tttttcatcc aaccatatgg gcggattact ttctcaaaca tgcttccaac tccaactcga     180
cgagttctga tggcgtagta gaggaacata ttgagagatt gaaaggagaa gtgaggaaga     240
tgttgatggg tgctatggat aagccatcgc aaaagttgaa cttgattgat cagatccaac     300
gcttgggatt tgcctaccat tttgaacatg agatagatga gcagctag                  348
```

<210> 112
<211> 508
<212> DNA
<213> Eucalyptus grandis

<400> 112
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cctctgctcc tcctcctccg ccgccacctc ctccacctcc tccggtgctc aattcgtgac     120
atgcactttg aagattgaag ctcaagagat cgggagacgg tcggcgaatt ggcaacctaa     180
cgtttttgac tacgactttc tgcagtcact caatgttgat tacacggagg ataaatactc     240
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gacggagatc aagaacgctc taagttccat ctataacaac gccgaagatg ctcaactttt     420
ggatgatctc tatgccgttt cccttcgatt ccggctactt agacaacatg gattcaacat     480
atcgcaagat gcgtttcaaa ggtttatg                                        508
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<210> 113
<211> 398

<212> DNA
<213> Eucalyptus grandis

<400> 113
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cctccccctc tgccgtttcc tcaggcactc ggtttgcgaa atgtgctttg actattgaag 120
atgaagatac cgcgagacgt tcggcgaatt ggaagcctag cgtttgggac tatggctttg 180
tgcagtcact caatactgat ttcccggtgg ataaatatac agagcaagtt caaaggttga 240
aggaagaagt caagggtcta ttccacaggg agatgaatca ggtggccaag ctcgagttca 300
ttgacgtggt tcaaagatta ggactaggat accattttga gacggagatc aataactctc 360
tcagttccat ctataacaac actgaagatg ttcaactt 398

<210> 114
<211> 432
<212> DNA
<213> Pinus radiata

<400> 114
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ttagccactt cgaagaattt caaatggcta gcgtttctgt taaagcggga gcaacttcta 120
ctgtgtcttg tgggttggcc agcaacaact tgatccgaag gacggccaat cctcatccca 180
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gtggagaatc aatgattact ccatctgctt atgacacagc atgggtagcc agggtgcctt 360
ccattgatgg ctctgcttgc cctcaatttc cccagacagt tgaatggatt ttgaaaaatc 420
aattaaaaga tg 432

<210> 115
<211> 363
<212> DNA
<213> Pinus radiata

<400> 115
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tcatcactca tacccatggc ctccgtcgtc gaccaagccg agctgtgcag caaatctgtg 120
agcatgagtt cacctggtgt acaaagacgc acaggcgatt accattccaa tctctgggac 180
gacgagttca tccagtccct ctcaacgcct tatggggcac cttcttaccg cgaacgtgct 240
gatagacttg ttggggaagt aaaggagatg ttcaattcac ttacagtact cactccccac 300
aatgatctcc ttgagcaact ttggatggtg gatagcgttg aacgtttggg aatcgatagg 360
cat 363

<210> 116
<211> 779
<212> DNA
<213> Pinus radiata

<400> 116
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caggcgatta ccattccaat ctctgggacg acgatttcat ccagtcactc tcaacgcctt 180
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tcaattcact tacactactc actcccctca atgatctcct tcaacgcctt tggatggtgg 300
ataccgttga acgtctggag atcgataggc atttcagaaa tgaaataaaa tcagcgttgg 360
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ctgatctcaa ctcaactgcc ttggggttcc gaactcttcg actacacgga tttccggtgt 480
cctcagatgt tttggaagtt ttcaaagatc aaaatgggaa gtttgcaggc tgctctgcca 540
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cctttcctgg ggagaaagtc atggaagagg ctcaaacatt ctgtacgtca tatttacaag 660
aagccctaaa aactgttccg atctccaatg atagtctttc acgagagatt gaatacgtta 720
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<210> 117
<211> 1173
<212> DNA
<213> Pinus radiata

<400> 117
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aatctctctt gagatggtgg aaagattatg gattccctga aataacattc tcacggcatc 180
gtcacgtgga atactacact ttagcagctt gcattgcaaa tgatcctaaa cattctgcgt 240
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tcaacgaaat ggcacgagag gcgcagaaaa ttcaaggctg ggatacagtc agctatgctc 480
gaaaatcttg ggaggctttt attggtgctt atatacaaga agccaagtgg atttccagtg 540
gttatcttcc cacgttcgac gagtacctcg agaatgggaa ggtcagcttc ggctctcgca 600
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acactcaatg ctacaaggct gacagggcgc gtggagaaga agcttcggcc gtatcgtgtt 780
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<210> 118
<211> 1634
<212> DNA
<213> Pinus radiata

<400> 118
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agcgcttccg ccaatgatac agagttgcag ataagaagcg tttttaattt atttcgagct 180
tctctcattg cttttcccga ggaaaaagtt ctggaagagg ctgaaaattt cgctgctgca 240
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gttttcgatt atcgttggca ctcaaatttg cctagactgg aagctaggag ttacgtcgac 360
atccttgcag ataatacgat cagtggaacg ccagatgcga acactaaaaa acttttagaa 420
cttgcgaaat tggagttcaa tattttccat tctctacaac agaaagagtt acaatgtctg 480
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gagtgcctac ctgaatatat gaaaggagtg tacagggtgc tttacgaaac cgtaaatgaa 780
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ccaacgtttc aggagtactt cgagaacggg aaactcagtt ctggtcatcg catagcgacg 960
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cttatgtaac cacatatcaa catagcagat ttacattaag ttgataccta gtctacgtta 1440
ctttaggtta tgtgttttat tattgtactt ttcagactct ttggtcgtat aggcctaggt 1500
tgcaaaggtg tttcaggacc ttgcgcatta atatagttgt caataatatg taagttatga 1560
attctcagtg aatacggttt gttatcagtt ttttggggaa tctaatttct attaagaaaa 1620
aaaaaaaaaa aaaa 1634

<210> 119
<211> 301
<212> DNA
<213> Eucalyptus grandis

<400> 119
gggaagtcaa ttatgggata ctgcatttgc tactcaagca attatctcaa ccaatcttat 60
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agaagattgc ccaggagacc taaatttctg gtatcgccac atctcaaaag gggcttggcc 180
tttttcgaca gcagatcacg gatggcccat ttcagactgc acagcagaag gattaaaagc 240
tgcccttgta ctatcaaaaa ttccattgga gattgttggg caaccattta gaagttatgg 300
g 301

<210> 120
<211> 433
<212> DNA
<213> Eucalyptus grandis

<400> 120
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aacaaggagc tctgagcgcg gccacccatc tcccggtttt cgctgggctt gcggcgagag 120
tctctctggg gttcctgggg cgtcgtttct tgatcgtggg atcaggatgt ggaaactgaa 180
agttgcggaa ggagcaaatc cttggctaag aagtctgaac aatcatgttg gtagacaaat 240
ttgggagttc gatccaaatt gtggatcccc agaagagatt caggagattg aagaggctcg 300
tgcaaacttc ttaaagcatc ggtttgagaa gaagcacagc tcagatttga tgatgcgaat 360
tcagttttcc aaggaaaata caggcagagt agttttacca ccagtaaagg tgaaagactt 420
ggatgaaatc aca 433

<210> 121
<211> 596
<212> DNA
<213> Eucalyptus grandis

<400> 121
gtaacgcaca tgttgagaag ggccataagc ttccattcaa ctcttcaggc ccatgatgga 60
cactggccag gggactatgg cggacctatg tttctcatgc ctggcttggt aattgccctt 120
tctattactg gagcactaaa tgccgtcttg tctgagcaac ataaacaaga gatgtgccga 180
tatctgtaca atcatcaaaa caaagatggc ggttggggtt tgcacattga aggtccaagc 240
accatgtttg gttctgtctt gaactatgtc acattaaggt tgcttggaga agctgcaaac 300
gatggacaag ggctatggga gaaggcacga aaatggattc tggaccatgg cagtgctact 360
gcaataacat catgggggaaa aatgtggctt tcagtacttg gagcatttga gtggtcaggc 420
aataacccat tgccccctga gatatggctt cttccttaca tgcttccgat tcatccagga 480
agaatgtggt gccactgccg gatggtttat ttgccgatgt catacttgta tgggaagagg 540
tttgtaagtc ccataacacc aaccgttttt gtccttgaaa aaaggaactt tatgca 596

<210> 122
<211> 332
<212> DNA
<213> Eucalyptus grandis

<400> 122
cactctcgac tctgcagttc ttggcacttt caaggtgcga gcttggtgtg ggcgtttgtt 60
tggcagataa atatacgaga gagagagaga aagagagaat gtggaagctg aagatagcgg 120
agggcgggcc gtggctgacc agcgtgaaca accacgtcgg gcggcagcat tgggagtttg 180
accctgacgc cgggacaccg gaggagaggg cggaggtgga gagggtccga gatgagttca 240
cgaggaaccg gttccgaatc aagcagagcg ctgatctttt gatgaggatg cagctcacaa 300
aggagaaccc aagcgggccg attcaccgcc gg 332

<210> 123
<211> 293

<212> DNA
<213> Eucalyptus grandis

<400> 123
attatgtctg ggttggggaa gatggaatta agatgcagag ctttggaagt caaatctggg 60
actgtggtct cagccttcaa gcgttgcttg caagcgatct cattgatgaa attggccccg 120
tccttaagaa aggacatgaa tttctgaagg aatctcagat cgaccgaaac ccctctggcg 180
acttaaagaa aatgtaccgt cacatttcca aaggagcatg ggctttctcg gacaaagatc 240
atggatggca agtttcggat tgcacagcag aaagtatgaa gtgttgccta gtt 293

<210> 124
<211> 604
<212> DNA
<213> Eucalyptus grandis

<400> 124
atcagtctcg tcatcagggg cagattcatc atggattcgc tttcctgaag acgcctcttc 60
catctctctg cctctctctc tctctctctc actccagcgc gctgactggg catttcggat 120
ccgtaccaga tggacacgga caacaaactc ttcaatgtgg gcgtcttgct cgtggccact 180
ctcgttgtgg ccaagctaat ctcggcgttg ctgattccga gatccggaaa gcgcctccct 240
cccgtcgtta ggacatggcc ggtggttggt gggctgctcc ggttcttgaa gggtccgatg 300
gtgatgctgc gggaagagta ccccaagctt gggagcgtat tcactctgaa tctgttgaac 360
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tccgatttga gccagcaaga agtgtaccaa ttcaatgtgc cgactttcgg acctggagtt 480
gtattcgacg tcgattacac catcaggcaa gagcagtttc ggttttttac tgaggctctg 540
aggattaata agctcaaggg gtatgtcaat cagatggtta tggaagccga ggactacttc 600
tcaa 604

<210> 125
<211> 515
<212> DNA
<213> Eucalyptus grandis

<400> 125
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tctctgcctc tctctctctc tcactccagc gcgctgactg ggcatttcgg atccgtacca 120
gatggacacg gacaacaaac tcttcaatgt gggcgtcttg ctcgtggcca ctctcgttgt 180
ggccaagcta atctcggcgt tgctgattcc gagatccgga aagcgcctcc ctcccgtcgt 240
taggacatgg ccggtggttg gtgggctgct ccggttcttg aagggtccga tggtgatgct 300
gcgggaagag taccccaagc ttgggagcgt attcactctg aatctgttga acaagaaaat 360
aacgttcttc atcggccctg aggtttctgc gcacttcttc aaggcttccg agtccgattt 420
gagccagcaa gaagtgtacc aattcaatgt gccgactttc ggacctggag ttgtattcga 480
cgtcgattac accatcaggc aagagcagtt tcggt 515

<210> 126
<211> 366
<212> DNA
<213> Eucalyptus grandis

<400> 126
gctgactggg catttcggat ccgtaccaga tggacacgga caacaaactc ttcaatgtgg 60
gcgtcttgct cgtggccact ctcgttgtgg ccaagctaat ctcggcgtct attccgagat 120
ccggaaagcg cctccctccc gtcgttagga catggccggt ggttggtggg ctgctccggt 180
tcttgaaggg tccgatggtg atgctgcggg aagagtaccc caagcttggg agcgtattca 240
ctctgaatct gttgaacaag aaaataacgt tcttcatcgg ccctgaggtt tctgcgcact 300
tcttcaaggc ttctgagtcc gatttgagcc agcaagaagt gtaccaattc aatgtgccga 360
ctttcg 366

<210> 127
<211> 458
<212> DNA

<213> Eucalyptus grandis

<400> 127
ttcttgaagg gtccgatggt gatgctgcgg gaagagtacc ccaagcttgg gagcgtattc 60
actctgaatc tgttgaacaa gaaaataacg ttcttcatcg gccctgaggt ttctgcgcac 120
ttcttcaagg cttccgagtc cgatttgagc cagcaagaag tgtaccaatt caatgtgccg 180
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cttgagcact tgaccatatt gacagcgagc agatgtcttt tgggtcgaga ggttcgtgag 420
aagctctttg atgatgtgtc agccctcttc cacgacct 458

<210> 128
<211> 442
<212> DNA
<213> Eucalyptus grandis

<400> 128
ctttgatgat gtgtcagccc tcttccacga ccttgacaat ggaatgctac cgatcagtgt 60
catcttcccc tacctgccca tcccagctca ccatcgtcgc gataaggctc ggaagaagct 120
ttctgagatt tttgcaaaca tcatttcttc acgaaaatgt gctggcaaat cagaagaaga 180
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ggtcactggt ctgcttattg cggctctctt tgcagggcag cacaccagtt ctatcacttc 300
cgtgtggact ggggcctacc tcctcaccaa caagaagtac ctctctgctg tctctaatga 360
acagaagcac ctgatggaga agcatgggaa caatgttgat catgatgttc tttctgaaat 420
ggatgtcctg tatcggtcca tc 442

<210> 129
<211> 392
<212> DNA
<213> Eucalyptus grandis

<400> 129
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gagaagcatg ggaacaatgt tgatcatgat gttctttctg aaatggatgt cctgtatcgg 120
tccatcaagg aagcactgag acttcaccca cctctaatta tgctgctccg aagctcgcat 180
agtgatttca gtgtcaaaac acgggatggc aaggaatatg aggtgggtga agtctcagtg 240
cttccttgat ggacccttga ggcaaggaaa ggtgtcggca aggcttttat cactgcattc 300
aggtcgggtg ccgtaatggg cttccttctt gctgcgaatg gtcttctggt cctttacatt 360
gccatcaacc tattcaagat ttacctatgg gt 392

<210> 130
<211> 354
<212> DNA
<213> Eucalyptus grandis

<400> 130
gttgtattcg acgtcgatta caccatcagg caagagcagt ttcggttttt tactgaggct 60
ctgaggatta ataagctcaa ggggtatgtc aatcagatgg ttatggaagc ggaggactac 120
ttctcaaaat ggggagatag tggcgaggtg gacctaaagt atgagcttga gcacttgacc 180
atattgacag cgagcagatg tcttttgggt cgagaggttc gtgagaagct ctttgatgat 240
gtgtcagccc tattccacga ccttgacaat ggaatgctac cgatcagtgt catcttcccc 300
tacctgccca tcccagctca ccatcgtcgc gataaggctc ggaagaagct tgct 354

<210> 131
<211> 442
<212> DNA
<213> Eucalyptus grandis

<400> 131
cttccgtgag aagaagggct ttggagatga caactggcag atgtctggat gggttgccct 60

tggatggatt tgattatgga tccatccttg gccaatgctg tgaactgcct attgggtatg 120
tgcagattcc tgtgggtgtt gcagggcctc ttctgcttga tggaattgaa aacatggttc 180
ccatggccac taccgagggc tgcctggtgg ccagcaccaa cagaggttgt aaggccattc 240
atatgtctgg gggtgctaca agcgttcttc ttagagatgg catgaccagg gctcctgtcg 300
ttcgattccc cactgctagg agagctgcac aactcaagtt ttacttggaa gccccaataa 360
ctacgaaagc ttgtctctca tcttcaacag cacccagcaa ggtttgccag gcttgcaaag 420
gaattcaagt gccgccaatt gg 442

<210> 132
<211> 984
<212> DNA
<213> Eucalyptus grandis

<400> 132
gtggcttctt attccctgga atcggctctt gggggagatt gcaggagagc tgctttggtg 60
agaagaaggg ctttggagat tagaactggg agatgtctgg atgggttgcc cttggatgga 120
tttgattatg gatccattct cggccaatgc tgtgaactgc ctgttgggta tgtgcagatc 180
cctgtgggtg ttgtagggcc tcttctgctt gatggccttg aaaacatggt tcccatggcc 240
accaccgagg gctgcctggt ggccagcgct aacagaggtt gtaaggccat tcatatgtct 300
ggtggtgcta caagcgttct tcttagagat ggcatgacca gagctcctgt agttcgattc 360
cccactgccg agagagctgc acatctcaag tcttacttgg aacatcccaa gaacttcgac 420
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gatatggatg ttattgctgt ttctggtaat ttctgtgccg acaagaaacc cacagctgtg 660
aactggattg aagggcgtgg aaaatccgta gtttgcgagg caattatcac tgaagcagtt 720
gttagcaagg ttttgaagac caccgttcca gctttgttag aattgaacat gctcaagaat 780
ttgactggat ctgcactggc tggtgccatg ggaggattca atgcccatgc atccaatatc 840
gtctcagctg tatttattgc aacaggtcaa gatcctgccc agaacattga gagctctcat 900
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<210> 133
<211> 527
<212> DNA
<213> Eucalyptus grandis

<400> 133
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ctggcagatg tctggatggg ttgcccttgg atggatttga ttatggatcc atcctcgggc 120
aatgctgtga attgcctgtt ggatatgtgc agattcctgt gggtgttgca gggcctcttc 180
tgctcgatgg ctttgaaatc atggttccga tggccaccac cgagggctgc ctggtggcca 240
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tcaagtttta cttggaacat cccaataact acaaaagctt gtctctcatc ttcaacagca 420
ccagcagatt tgccaggctg caaggaatca agtgcgcaat tgcaggaagg aatctgtaca 480
tgaggttttg ttgttccact ggagatgcca tgggggatga atatggg 527

<210> 134
<211> 965
<212> DNA
<213> Pinus radiata

<400> 134
aaacaaccag ccgagttcga aggtggtcaa cccacgtgta ccatcatggc acgtaagtag 60
atggcgaaaa tgttggaagg ccagttgtag tgaccagggg aatttaaaat tattaatacg 120
ggactataaa taactagcag caatctctgg cttttccact gcattcatac cgggagtttg 180
gggggattcc aaaggatttc ttcctctctc tctccagtcc tcaatggatg gccttgtgct 240
gaggaaaaca agaaaattta gtggagaaat ggattgttgc tccaacaaga agatggagga 300
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gacattggca tctgatgcct tgccattgcc tgtgggacta accaacaagg ttttctttat 420

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ccaatgctgt gaactgcctg ttgggtatgt gcagattcct gtgggagttg caggacctct 960
tcttc 965

<210> 135
<211> 503
<212> DNA
<213> Pinus radiata

<400> 135
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tctcccggag cgaatgctcg gctcttggcc aggattgtag caggagcagt tttggctgga 180
gagctctctc tcatgtctgc tttggctgca ggccagctgg tcaagagcca tatgaagtac 240
aacagatcaa tcaaggatat caaagcaatc tcctgaacct catggtcctt agaatccaag 300
aaagtcagca tggtttttct ccattgcgta tctttactat agcaatagac ttatttgatc 360
aagctagggt cctccaaaag aaagtttcgt acctgttacc tgttttgcat tgcatatgtt 420
atttgatcag ctggggtcct ccaaaaggaa gtttcctacc tgctttcaat tgcatatgtt 480
atttgatttt catccaagtt cta 503

<210> 136
<211> 563
<212> DNA
<213> Pinus radiata

<400> 136
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acagcaaaac aacaacatat ttacaagcag taaaatccac cctgtagtga tagtcccagg 120
cacaggagga aatcaggttg aagcaaggct aactgcagac tataaaccca gtgggctgtt 180
gtgcagaagg tggaattggg agagggagtg gttcagaata tggtttgatg ttcctgtcgt 240
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agatgaatac tacaatgccc ctggggtgga gactagagtg ccttattttg gttcaacaga 360
aggaatgaag taccttgatc cctgcttcaa gtatataacg ccatacatgt catccttggt 420
gaaatctctt gaggatgttg gatatgttga cggtaaatcc ctttttggtg caccctatga 480
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gagaaaattg gtggaggagg cgt 563

<210> 137
<211> 354
<212> DNA
<213> Pinus radiata

<400> 137
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tgcaccgtct tcgactgatt caggctcctc tggaaatgta gttattgatt tctattgggg 120
tatggagctt tatcctcgaa taggtaaaaa ctttgacatc aaggtcttca caaattgtcg 180
gtttggaatg atgtcttggg cagttcttgc agtaacatac agcataaaac agtatgaaga 240
gtatggaaga gtagcggatt ccatgttagt aagcagtata ttgatggtgg tgtatgtaac 300
aaaagttctt cttgtgggaa tctggctact ggaacaccat ggatataact catg 354

<210> 138
<211> 631
<212> DNA
<213> Pinus radiata

<400> 138
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atggttgaag actatggcaa ctattggata cacaggtggc tacattgcaa atggggctat 180
gagaagatcc atcatgttca ccatgagttc actgctccaa tgggttttgc tgctccatat 240
gcacattggt cagaggtgtt gatattgggg atccctacgt ttgtcggacc ggcaattgct 300
ccaggacaca tgattacatt ctggtgctgg gttgtgctgc gccaagtgga agcgattgaa 360
actcacagcg gatatgactt tccgtggact cttaccaaat taattccttt ctatggaggc 420
gcggagtatc atgactacca tcattatgta ggaggacaaa gtcaaagcaa ctttgcctca 480
gtgttcacat actgtgatta tttatacggg actgataagg gttaccgcta tcgtaaggag 540
catcttttga aggcacgtga gtttgaatat aggttaaagc agatgatttt aagaaagaaa 600
acggcaatgg agcagtttca gataagtttg t 631

<210> 139
<211> 362
<212> DNA
<213> Pinus radiata

<400> 139
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ggcacattgt ggttatgatt ttccttggag catttcaaag ctattcccgt tgtatggagg 120
agctgatttc catgattatc atcatcgact gctctataca aagtctggga attactcatc 180
gactttcact tacatggact ggttatttgg gactgataaa gggtaccgga agctaaaagg 240
tctccagaaa gattctaaat gataacccaa gagtgccatc aaacatttgt gtatgtgtgt 300
atcaattggt tgaaggaaga gaacagcaca gacaggccta gatcactctc agtgagttcc 360
ag 362

<210> 140
<211> 504
<212> DNA
<213> Pinus radiata

<400> 140
tctcgctcat cctatcctag ttgggcgaaa gaataacttc tcactggagt ggattcgatt 60
tcaccagatt gggatttgtc atggcgacat tggtggaaag aggctggctg tatctgatca 120
caaatttcac tgatttttcaa ctggcttcca taggcagttt tcttcttcat gagagcatct 180
tctacttgtc tgggcttcct ttcatattac ttgagactac aggcttgttg agcaagtaca 240
aaattcagag caagacgaac acagttgctg cacaagaaaa atgtattact cgactgctgc 300
tatatcattt ttgtgtcaac ctgccagtca tggtggtttc ctatcctgta ttcagattta 360
tgggcatgac aagcgtgcta ccactaccat cctggaaagt agttgtatcc caactggttt 420
gttatttcat tttggaggat tttgttttct actggggcca cagaatttta cattcaaaat 480
ggctgtacaa gcatgttcac agtg 504

<210> 141
<211> 1293
<212> DNA
<213> Pinus radiata

<400> 141
caagtactct ttataagctc tgaatgattg ctagctcaaa taggcaacga agaattgctt 60
gtaaactatt cctgagaagt gtgtctgtta cacaattctc aaatatcatt gatcttcagg 120
attttggatc acatctgaga acccaggtat gggagaagag ttgcagacat ggatattaat 180
ggtcactgct agagctccta caaatatagc agtgatcaag tactggggga aaagagatga 240
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agccacaacc actgtagcag ttagcccatc attcacatct gatagaatgt ggctcaacgg 360
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gggaaatgat gtagtggacg agaagaaggg aattgttatc aggaaagagg attggcagag 480
gcttcacttg catattgctt cgtataataa tttcccaact gcagctggct tggcttcttc 540
ggctgctgga ttcgcttgtc tagtttatgg tctggcaaaa ttaatggacg tcaaggaaaa 600
atatcagggg gaactttcag ccattgcccg ccgaggttca gggagtgcat gccgtagcct 660

ttatggtgga gtggtaaaat ggatgatggg aaaggaaacc gatggaagtg acagcattgc 720
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gattattaac tgtattgaaa gatggaatcg gtctgaagga actccacagg ttgcatatac 1080
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tcttcagcga ctgcttttct attttcctcc ggactccagc aaaacattgt caagttatgt 1200
gataggcgac acctcaatac taggagaaat cggcgtggac tcaatgaagg atgttgaatc 1260
cttgactgct cctccagagc tcaagagtga aag 1293

<210> 142
<211> 389
<212> DNA
<213> Pinus radiata

<400> 142
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tggatcacat ctgagaaccc aggtatggga gaagagttgc agacatggat attaatggtc 180
actgcaagag ctcctacaaa tatagcagtg atcaagtact gggggaaaag agatgaaaag 240
ctgatccttc ccatcaatga cagcatcagc tttactttgg atccagacca tctgtcagcc 300
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gaggtctctc ttggagggga gagatatca 389

<210> 143
<211> 693
<212> DNA
<213> Pinus radiata

<400> 143
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gaacagagaa gggcttaaca cgatattgcc tgaggaccaa gtctataaga tagaccagga 120
tagctatgcc tctcactctt ctattggcga atacatgggc atcgtctgcc atagtttcca 180
ggagggtatc gctctttgtg gcttgctcaa caactgtagt ctctcgttca ttcagtaaga 240
gctgctccgg tgctataccc cggaagccca aatctgctca tcccgcactc actgggagca 300
gaacttgctt ctcccggaac ccaattgtta gaaatttgat tggatccgct tctaagatgg 360
gcgcgacagt ggaggatacg accatggatg ctgttcagag gcggctcatg ttcgaagatg 420
agtgcatttt ggtggatgaa gaggatcatg tcattgggca tgactcaaaa tacaattgtc 480
acttgatgga gaaaatagag tcagagaatc tattgcatag agctttcagt gtgtttctat 540
tcaatacaaa atatgaattg cttcttcagc aacgttctgc aacaaaggtg acattccctt 600
tggtatggac aaatacctgc tgcagccatc ctctctacag ggagtctgag ctcattgagg 660
agaacaattt agggtcagaa atgcagccca aag 693

<210> 144
<211> 385
<212> DNA
<213> Pinus radiata

<400> 144
cgcctgcagg tcgacactag tggatccaaa gaagaactgg tgtgatggca ggaattccag 60
tcctaaggcc attttgcatc tgtttgcttt cagtctacat gctgcacatt gtagctgcag 120
tagcttcacc aaggctaggt agaagcagct tcccaagggg tttcaaattt ggtgcagggt 180
catctgctta tcaggcggaa ggagctgctc atgagggtgg caaaggccca agcatttggg 240
atacattctc ccacactcca ggtaaaatcg ctgatgggaa gaatggggat gttgcagtag 300
atcaatacca ccgttataag gaagatgtgc agcttctcaa atacatggga atggacgtct 360
atcgtttctc tatctcctgg tcacg 385

<210> 145
<211> 385

<212> DNA
<213> Pinus radiata

<400> 145
aaggccccag catttgggat acattctccc acactccagg taaaatcgct gatggaaaga 60
atggggacgt tgcagtagac caataccacc gttataagga agatgtgcag cttctcaaaa 120
acatgggaat ggacgtctat cgtttctcta tctcctggtc acgcatattt cctaaggggt 180
cgccaagaca cggaccagtc aataaagtgg gaatcgttta ttacaataat ttcatcaacg 240
agctgctcag gaatggtata gagccttttg tcacactgtt tcactgggac atgccacaag 300
ctctggaaga tgagtacggg ggattccgta acaaaagagt cgtggaggac tttaacatat 360
ttgcagaagc atgctttcga gcctt 385

<210> 146
<211> 546
<212> DNA
<213> Eucalyptus grandis

<400> 146
ctcccctgtc cttttcctcc tcccttcatt aattctctct tccgagatct gattttccct 60
cactttcccg agaaaataat ccccccgatc tccccccggg aattcccccc cggccgttcg 120
attccggcgc gcgctccggc gatcgctcgc tcgctcgcta gccggttctt ctctcgctcg 180
ttccaccgga gatggcgggc gaatggatac tgacgttgac cgcgcagacg ccgacgaaca 240
tcgcggtgat caagtactgg gggaagcggg acgagtccct catcttgccc gtgaacgaca 300
gcatcagcgt gaccctggat cccgggcacc tctgcaccac caccaccgtc gccgtcagcc 360
ccgccttcga gcaggaccgc atgtggctca atggcaagga gatatctctt tctggagata 420
gatttcagag ttgtttgaga gaaattcgag cccgtgctac tgacgttgag aataaggaaa 480
aaggaattaa aatttcaaag aaagattggg agaaactgca cctccacatt tctttcttta 540
catttc 546

<210> 147
<211> 786
<212> DNA
<213> Pinus radiata

<400> 147
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ggctctctcc aggtacctgg ttcgcttcct ctgcatgttt tttagaccaa tagtttcccg 120
acttacggaa tttggcttag aattaggccc tgcaaaagtt ttatagcttc ctctggggta 180
acggtagctt acagggttga attcgttgga gcatcggtga gaagctacag acatgagtag 240
caatggcaac gggcaaaaac aaggaggggg ctttttcgcc gccttcgcct cgggcctctc 300
taatttcgga agcgcgatgc acaaatcggt taacagcttc atgggatatg agggtttaga 360
agtagtcaat cctgaaggcg gtcaggatga tgcagaggag gaagctcatc gaggtagatg 420
gcggaaagag gaccaggata gttattggaa aatgatgcaa aaatatattg gagcagatgt 480
cacctccatg gtgacacttc cagtcattat ctttgagcct atgacgatgc ttcagaagag 540
tgctgagtta atggagtaca cttatttgct tgacatggca gatgagtgtg aagatcccta 600
tctcaagatg gcttatgcag catcatgggc aatttctgtc tatcctgcat accagaggag 660
ttggaagccc tttaacccta ttcttggaga aacttatgaa atggtcaatc atggagggat 720
cacatttatc gcagagcagg tcagccacca tcctccatgg gctcagccta tgccagaaat 780
gacatt 786

<210> 148
<211> 1748
<212> DNA
<213> Pinus radiata

<400> 148
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agaagctaca gacatgagta gcaatggcaa cgggcaaaaa caaggagggg gctttttcgc 120
cgccttcgcc tcgggcctct ctaatttcgg aagcgcgatg cacaaatcgg ttaacagctt 180
catgggatat gagggtttag aagtagtcaa tcctgaaggc ggtcaggatg atgcagagga 240
ggaagctcat cgaggtagat ggcggaaaga ggaccaggat agttattgga aaatgatgca 300

aaaatatatt ggagcagatg tcacctccat ggtgacactt ccagtcatta tctttgagcc 360
tatgacgatg cttcagaaga gtgctgagtt aatggagtac acttatttgc ttgacatggc 420
agatgagtgt gaagatccct atctcaagat ggcttatgca gcatcatggg caatttctgt 480
ctatcctgca taccagagga gttggaagcc ctttaaccct attcttggag aaacttatga 540
aatggtcaat catggaggga tcacatttat cgcagagcag gtcagccacc atcctccaat 600
gggctcagcc tatgcagaaa atgaacattt tacatacagt ctgtcctcaa aagtaaaaac 660
caagtttctt ggcaactctg tggatattta cccacttgga aggacacgtg tggtgctaaa 720
gaaatccgga gacgttctag atttggtgcc gcctccatct aaagttcata acctaatttt 780
tggacgaact tggattgatt cacctggtga gatggtgctg acaaatttga ctacgggaga 840
taaagtggtg ttgtactttc aaccatgtgg ctggtttgga gctggtcgct atgaagtgga 900
tgggtatgta tatgattcca aggaagaacc taagatattg atgacaggaa aatggaatag 960
atcgatgggt taccagcctt gtgatgctga aggggagcca cttcctggca cagagcttaa 1020
agaggtatgg agggtcgcag atcttccaaa gaatgacaaa tttcaatata catatttgc 1080
acacaaaatt aacagttttg atacggcacc aaagaagctg cttgcatcag attctcgtct 1140
tcgtcctgac cgtagtgcac tagagatggg agatctgtcg aaggctggag ctgaaaaatc 1200
caatcttgag gaaagacaac gggcagaaaa gagatgtaga gaggaaaaaa atcaaccttt 1260
cactcctagg tggttcacag taactggaga agttgccact acgccttggg gtgatttgga 1320
agtgtatgaa tataatggta aatattccga acatcgtgct tcagtcgatg actctaattt 1380
tgatgacgga acagattcaa aatctatgga gttcaaccca tggcagtatg gaaacattga 1440
gtctgggagc aacaaaaagg ttgaatgaca tcctcgtgct cgaaaatagc atgatctctt 1500
aattctttcc ttgtaatgtt atgattctga tggaattttg ctgcttttct cttgtggggt 1560
ttatgtcatc ttcattttgc taatgtattt tgaactcaag ttaacagacg atggaaacaa 1620
acttccgtgc catgagttga atgaaatttt aaaagataat ggaagctgcc tccatgtgat 1680
cagaaacttg gcatataatt gatatcatgt acctatgttt tggtttgggg aagaaaaaaa 1740
aaaaaaaa 1748

<210> 149
<211> 428
<212> DNA
<213> Pinus radiata

<400> 149
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gcttcctctg ggtaacggt agcttacagg gttgaattcg ttggagcatc ggtgagaagc 120
tacagacatg agtagcaatg gcaacgggca aaaacaagga gggggctttt tcgccgcctt 180
cgcctcgggc ctctctaatt tcggaagcgc gatgcacaaa tcggttaaca gcttcatggg 240
atatgagggt tagaagtagt caatcctgaa ggcggtcagg atgatgcaga ggaggaagct 300
catcgaggta gatggcggaa agaggaccag gatagttatt ggaaaatgat gcaaaaatat 360
attggagcag atgtcacctc catggtgaca cttccagtca ttatctttga gcctatgacg 420
atgcttca 428

<210> 150
<211> 419
<212> DNA
<213> Pinus radiata

<400> 150
gaaaatgaag gctcaattat ctcgtcctta tatctcagct gagggttgga atggacttat 60
ccaaagtaac atttccaaca tttgttctgg agccgcggag catgctcgaa cgtatcacgg 120
atttcatgtc gcatcctgat ttgatcttcg gggctgagaa tagcaatgat cctgaagaac 180
gattcatgcg cgtactgtca tactatttgg ctggttggca tattaagcca aaaggcgtca 240
aaaaaccgta caatccagtt cttggcgagt tttccgctg tagatatgac tattcgaata 300
atacacaagg tttttatatt gctgaacaag tctctcatca tccccccatt tctgcatttt 360
tctacatttc tcctgccaac cgcgtgagca tcatcgggga actaagacca aagtcaaag 419

<210> 151
<211> 401
<212> DNA
<213> Eucalyptus grandis

<400> 151

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cttcatctaa agggcggcat tgcaaaccct tcaacccttt actgggggaa acttatgaag     60
ctgactatcc ggagagagga gttcacttct tttccgagaa ggttagtcac caccctactc    120
tcattgcttg ccattgcgaa ggaaggggtt ggaaattctg ggctgacagc aatttaagga    180
caaaattttg gggacaatct attcagcttg atcctgtggg agcacttacc cttgagtttg    240
atgatggcga gatttttcaa tggaataagg taacaactag catcaacaat cttatcattg    300
gaaaagttta ctgtgatcat catggtgtca tgaatataca tggtaaccac caatattcat    360
gcaaattgaa gttcaaggag ccatctattc ttgccgaact c                        401
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<210> 152
<211> 349
<212> DNA
<213> Eucalyptus grandis

<400> 152

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cgcacatgcg attggtctat gcgggcatca tgggctatat cagtctatta tgcctatcaa     60
aggacgtgga agcctttcaa tcctattctt ggggagactt atgaactggc aaatcatggc    120
ggtattactt ttattgctga gcaggtctgt catcatcctc caatgagtgc cgggcatgcg    180
gaaaatgatc attttacgta tgatgtgaca tcaaaattaa aaaccaaatt cttagggaac    240
tctgttgatg tttatcctgt aggaagaaca cgtgtcactc ttaaacgaga tggtgtggtt    300
ttagatttgg tgccaccccc aacaaaggtt aacaacctga tttttggac                349
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<210> 153
<211> 533
<212> DNA
<213> Eucalyptus grandis

<400> 153

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ctctcgttta cgtcctgata gatatgcact tgagccgggt gaccttccta aagctggtgc     60
tgaaaagagc agcttggagg aaaggcaaag aggagagaaa aagaaccgag aaatgaaagg    120
ccagaaattc actccaaggt ggtttgatct gactgacgaa attagtccca caccttgggg    180
cgatttggaa gtgtaccgct acaatggaaa gtatactgaa catcgggctg ttgtagacag    240
tctagacacc atcgaagagt ctgacattca atcaactgag ttcaatccct ggcagtacga    300
ggcaactttt gctgaataag ttatctagtg caaattctac ttcctgaata cttctttttc    360
acctcctttt tcttacgtag tggccaatgt atatcatagt tgatcgtctt gaatgcgatt    420
agcatgttat tcgccccttc gttcttctac tcagcatttt tttattcata ggagatcgta    480
ttgtataatt taccgctgca ctgcagcatg gtgtttaaat agtcagttga gat           533
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<210> 154
<211> 354
<212> DNA
<213> Pinus radiata

<400> 154

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ggttcttcga ggcctcgaca ctgttgagga tgatacaagc attccattgg atacaaagct     60
accaattctg aaggctttct ataaacacat atatgatcct tcctggcact tttcatgtgg    120
agtcgagcac tacaaagaac tgatggaaaa atttcatcat gtttcaacta cctttttacg    180
gcttggaagg ggatatcagg aagcaattga agaaataact aagaagatgg gtgctgggat    240
ggcaaaattt atctgcaaag aggttgaatc agtggaggac tatgatgaat attgccatta    300
tgtcgcagga ctagttggat ttggtttgtc acgactcttt catgcagctc agct          354
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<210> 155
<211> 675
<212> DNA
<213> Pinus radiata

<400> 155

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ctcaaaaccg taaacgctct ggccacgtca ctcgtgagta accctccaat gccttacgac     60
agattcaggt caggtcatta attgcaggaa tcggtacact gccatggcaa tctatacgcc    120
tcaaccagca catcgactga tatcgtggtc tacaatggag aatcatacgg tggtgattgc    180
ggcagccatt agctttgttt ctgtattatt gtcgtattat atagttttga gcaggtggaa    240
gcgcagatcc aacggattac ggggaataca gagcaaaagt ttcgaaaagt caacagatga    300
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caatggcatt gccatcgaag ctgctggagg aacggatgtt atcatcgtgg gagcaggagt 360
cgcgggttcg gctctggctt acacacttgg caaggatgga agacgtatac atgtaattga 420
gagagacttg agtgagcctg accggattgt aggggaactt ttacagccag gtggatattt 480
gaaattgatt gagctgggac ttcaagattg tgttgaagga attgatgccc agagtatatt 540
tggggatgct ttattcaagg aaggaaaaga tactaaagtg gcatatccgt tagaaaacca 600
ccatgcagat agagctggaa ggagtttcca caatggacgc ttcatccagc gcatgcggga 660
aaaggctgct tcact 675

<210> 156
<211> 373
<212> DNA
<213> Pinus radiata

<400> 156
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atctatacgc ctcaaccagc acatcgactg atatcgtggt ctacaatgga gaatcatact 120
gtggcgattg cggtagccat tggctttgtt tctgtattat tgtcgtatta tatagttttg 180
aacaggtgga agcgcagatc caacggatta cggggaatac agagcaaaag tttcgagaag 240
tcaacagatg acaatggcat tgccatcgaa gctgctggag gaacggatgt tatcatcgtg 300
ggagcaggag tcgcgggttc ggctctggct tacacacttg gcaaggatgg aagacgtata 360
catgtaattg aga 373

<210> 157
<211> 522
<212> DNA
<213> Eucalyptus grandis

<400> 157
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gcaagagccg agctccatcg gcggacgttt ctcgatctct ctgctgtcgc gtggcggagg 120
ttggtggagc tgttaagccg gatcggtctc tgatggacgg tcagtacttg gtcagtggcg 180
tcttggctct gttcctgggg atcttcctgc tgtacaaggg gctcgggaag cagaagagga 240
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tgcccggcgg cgtcgatggg agcaccgaca tcgtcattgt cggagcaggc gtcgccggtg 360
cggctctcgc ttacgccctc gggaaggatg gacgtcgcgt gcgtgtaatt gagagggacc 420
tgacggagca agatagaatt gtcggcgagc ttcttcaacc aggaggttac ctgaaattga 480
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<210> 158
<211> 898
<212> DNA
<213> Eucalyptus grandis

<400> 158
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ataattaagg cattaacgga taccggacaa agagggatag ttggtcgagg ttggggtgat 180
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ggactaaaag cagggtgtcc tacaaccata gttcctttct ttggggatca gttcttctgg 360
ggcgataggg tccaccaaag aggccttggc cctgcaccaa taccaatctc ccagctcagc 420
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catcggcatc tgcccgaaga gtttccctcg tcgagtgtgt cctcggacgg tgaggagcac 600
cccaacccct tcctgtggct cttcctccaa gttgagaagt ggtgctgcct gccatgtagt 660
aaataggggc cttcctttgg ataaattgag agtgggtgta tagaagtgat agatgtcttc 720
cttattgttt tctgtccctc agttaccatt tttttttct ttcaaatttg tttcaaatca 780
ttcatttcat tcttatcagg gtttggctga ccattgtatt cagcatagca taagatttaa 840
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<210> 159

<211> 342
<212> DNA
<213> Eucalyptus grandis

<400> 159
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tttggggatc agccctttg gggagaacgg gtgcatgcaa ggggggtggg cccagtgcca   180
attccagttg atgaatttc tcttgaaaag ttggttgatg caatacgttt catgcttgat   240
ccaaaggtga aacagtgtgc agaagaacta gccaaagaca tggaacatga agatggagtg   300
gagggagcag tgaaggcttt ctacaaacac tttccacgcg aa                      342
```

<210> 160
<211> 582
<212> DNA
<213> Pinus radiata

<400> 160
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cttatgatcc cctaacccct aaatcgtagc agtgaagcca ttaacgattt ttgcgggttc   120
agaaagattc actgaatcgc ttactaaaac tctgtttcag gaatggcaac aggaggagga   180
gcgttggatc tggcctcagg aatgggaggc aacattgaga aagaacaaat gctgaccgct   240
gttgaagagt acgaaaaata tcacatgtac tatggtggtg atgaaggctc gagaaaatct   300
aactatacag acatggtaaa taaatactat gatctggcga ctagtttcta tgagtatgga   360
tggggggagt cttttcattt tgctcacaga tggaaagggg agaccctccg agaaagtata   420
aagcgccatg aacattttct tgctcttcac ctttgtttaa agcctgcaat gaaggtattg   480
gatgttggat gtgggattgg aggtccactg agagaaattg ctaggttcag tcggacttcg   540
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<210> 161
<211> 552
<212> DNA
<213> Eucalyptus grandis

<400> 161
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tggcgacggg ccttggcggg aagatggaca agagcgacgt cctgtccgcc gttgacaagt   180
atgagaagta tcatgtctgc tatggaggtg atgaggaaga aaggagagct aactatagtg   240
acatggtgaa taaatattat gatcttgcta ccagctttta tgagttcggc tggggagaat   300
ctttccattt tgcccacaga tggaaagggg agtctctacg agagagcatt aagagacatg   360
aacactttct tgcattacag ctaggcttaa aacctgggca caaggtgctg gatgtcgggt   420
gcggaattgg tggaccgctt agggaaatag ctcgattcag ctccgcatct gttacaggat   480
taaacaacaa tgagtaccag ataacaaggg gaaaggaact aaaccgcatt gcaggcgtgg   540
acaagacatg cg                                                       552
```

<210> 162
<211> 401
<212> DNA
<213> Eucalyptus grandis

<400> 162
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ggatctggcg acgggccttg gcgggaagat ggacaagagc gacgtcctgt ccgccgttga   180
caagtatgag aagtatcatg tctgctatgg aggtgatgag gaagaaagga gagctaacta   240
tagtgacatg gtgaataaat attatgatct tgctaccagc ttttatgagt tcggctgggg   300
agaatctttc cattttgccc acagatggaa aggggagtct ctacgagaga gcattaagag   360
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<210> 163

<211> 446
<212> DNA
<213> Eucalyptus grandis

<400> 163
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gacgaaatgc ttttcaagaa taagcgatgt tggttggctt gcttacctag tgtacttgtc  120
aatatatctt gtaatggcgg agtttgggat atattggatg cacagagagc tgcatgacat  180
taaacccctt ta[illegible]ct  240
ttctcctttt gccggcttgg cgtttcatcc tctagacggg atactgcagg cggtgccaca  300
tgttatggca ttattccttg [illegible]ctttttct  360
cgaggccata tggacagcaa atatccatga ctgcatccat ggtaagcttt ggcctgtgat  420
gggcgctggt tatcacacca tccacc                                        446
```

<210> 164
<211> 823
<212> DNA
<213> Eucalyptus grandis

<400> 164
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gggtgcaatt gttcggacag acaagtctct cagtcaaggg atccccattg agattggaaa  180
ggggagaatt cttgcagaag gtaaagatgt tg[illegible]tt ggttatgggt caatggttca  240
gaactgtgtc aaagctcggt cccttctttc aaagctcgga attgaggtga cagtcgctga  300
tgcaagattc tgcaaaccgc ttgacatagg attacttagg gagttgtgtg aaaatcatgc  360
ctttctggtc actgttgagg aaggatccat cggaggtttc gggtcccatg ttgcacagtt  420
cattgcactt gatggacggc ttgatgggag aataaagtgg cggccgattg ttttacctga  480
tgccta[illegible]  540
tcacattgcc gcaactgtgt tgagtctcct tggccggaca cgcgaagctc ttctgttgat  600
gtgctaggtt ccctgcaatt cttccgccc[illegible]gaaatgggct cgtgctgatg  660
ccgcagtact gataagccag acatgttaat gaagcttgag caaagatggc ttactcgccg  720
actaccatgt gtccagaatg ctgtgttgat tgttggcatg cagtacgttc tatcgccaga  780
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<211> 90
<212> PRT
<213> Eucalyptus grandis

<400> 165
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Pro Ile Ser Val Ile Phe Pro Tyr Leu Pro Ile Pro Ala His His Arg
            20                  25                  30
Arg Asp Lys Ala Arg Lys Lys Leu Ser Glu Ile Phe Ala Asn Ile Ile
        35                  40                  45
Ser Ser Arg Lys Cys Ala Gly Lys Ser Glu Glu Asp Met Leu Gln Cys
    50                  55                  60
Phe Ile Asp Ser Lys Tyr Lys Asn Gly Arg Pro Thr Thr Glu Ala Glu
65                  70                  75                  80
Val Thr Gly Leu Leu Ile Ala Ala Leu Phe
                85                  90
```

<210> 166
<211> 40
<212> PRT
<213> Eucalyptus grandis

<400> 166
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Tyr Leu Leu Thr Asn Lys Lys Tyr Leu Ser Ala Val Ser Asn Glu Gln
```

```
1               5                   10                  15
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            20                  25                  30
Ser Glu Met Asp Val Leu Tyr Arg
        35                  40

<210> 167
<211> 167
<212> PRT
<213> Eucalyptus grandis

<400> 167
Arg Leu Asn Glu Ala Glu Gly Glu Asp Gly Pro Tyr Leu Tyr Ser Thr
1               5                   10                  15
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            20                  25                  30
Thr Ala Gly Glu Arg Ala Glu Val Glu Ala Ala Arg Gln His Phe Tyr
        35                  40                  45
Asp His Arg His Gln Val Lys Pro Cys Gly Asp Leu Leu Trp Arg Met
    50                  55                  60
Gln Phe Leu Arg Glu Lys Glu Phe Lys Gln Thr Ile Pro Pro Val Arg
65                  70                  75                  80
Val Glu Asp Gly Glu Glu Ile Thr Tyr Asp Lys Ala Ser Thr Ala Leu
                85                  90                  95
Lys Arg Ala Val His Phe Phe Ser Ala Leu Gln Ala Ser Asp Gly His
            100                 105                 110
Trp Pro Ala Glu Asn Ala Gly Pro Leu Phe Phe Leu Pro Pro Leu Val
        115                 120                 125
Met Cys Val Tyr Ile Thr Gly His Leu Asp Ala Val Phe Pro Ala Glu
    130                 135                 140
His Arg Lys Glu Ile Leu Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp
145                 150                 155                 160
Gly Gly Trp Gly Leu His Ile
                165

<210> 168
<211> 89
<212> PRT
<213> Eucalyptus grandis

<400> 168
Met Asp Asp Ile Val Ser His Glu Phe Glu Gln Lys Arg Gly His Val
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            20                  25                  30
Glu Ala Val Glu Glu Leu Gln Lys Arg Val Ile Asp Ala Trp Lys Asp
        35                  40                  45
Thr Asn Glu Glu Phe Leu Arg Pro Ile Ala Val Pro Met Pro Ile Leu
    50                  55                  60
Thr Arg Val Leu Asn Leu Ser Arg Val Ile Asp Val Leu Tyr Ser Asp
65                  70                  75                  80
Gly Asp Asn Tyr Thr His Ser Glu Thr
                85

<210> 169
<211> 
<212> PRT
<213> Eucalyptus grandis

<400> 169
Met Glu Asp Asp Arg Gly Leu Leu Tyr Asp Ser Asp Pro Pro
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Ser Pro Ser Leu Ser Pro Pro Leu Ser Pro Pro Arg Pro Phe Ala Leu
            20                  25                  30
Thr Phe Phe Asp Arg Glu Arg His Val Thr Phe Leu Glu Met Met Tyr
        35                  40                  45
His Met Leu Pro Arg Pro Tyr Gln Ser Gln Glu Ile Asn His Leu Thr
    50                  55                  60
Leu Ala Tyr Phe Val Ile Ser Gly Leu Asp Ile Leu Asp Ala Leu Asp
65                  70                  75                  80
Arg Val His Lys Asp Ala Val Ala Asp Trp Val Leu Ser Phe Gln Ala
                85                  90                  95
His Pro Arg Ser Lys Ala Asp Leu Asp Asn Gly Gln Phe Tyr Gly Phe
            100                 105                 110
His Gly Ser Arg Ser Ser Gln Phe Pro Ser Lys Asp Ala
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<210> 170
<211> 119
<212> PRT
<213> Eucalyptus grandis

<400> 170
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            20                  25                  30
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        35                  40                  45
Arg Pro Tyr Gln Ser Gln Glu Ile Asn His Leu Thr Leu Ala Tyr Phe
    50                  55                  60
Val Ile Ser Gly Leu Asp Ile Leu Asp Ala Leu Asp Arg Val His Lys
65                  70                  75                  80
Asp Ala Val Ala Asp Trp Val Leu Ser Phe Gln Ala His Pro Arg Ser
                85                  90                  95
Lys Ala Asp Leu Asp Asn Gly Gln Phe Tyr Gly Phe His Gly Ser Arg
            100                 105                 110
Ser Ser Gln Phe Pro Ser Lys
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<210> 171

<213> Pinus radiata

<400> 171
Leu Ile Ala Phe Pro Gly Glu Lys Val Leu Glu Glu Ala Glu Ile Phe
1               5                   10                  15
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            20                  25                  30
Leu Ser Arg Glu Ile Ser Tyr Val Met Glu Tyr Gly Trp His Ile Asn
        35                  40                  45
Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Phe Gly Gln Asp
    50                  55                  60
Pro Ile Tyr Leu Met Pro Asn Met Lys Thr Gln Lys Leu Leu Glu Leu
65                  70                  75                  80
Ala Lys Leu Glu Phe Asn Met Phe His Ser Leu Gln Gln Gln Glu Leu
                85                  90                  95
Lys Leu Leu Ser Arg Trp Trp Lys Asp Ser Gly Phe Ser Gln Met Thr
            100                 105                 110
Phe Pro Arg His Arg His Val Glu Tyr Tyr Thr Leu Ala Ser Cys Ile
        115                 120                 125
```

1. INTRODUCTION

The Intellectual Property Office is part of the Business and Registries Branch. The Intellectual Property Office administers legislation for providing the protection of intellectual property rights by granting patents under the Patents Act 1953 and registering trademarks and designs under the Trademarks Act 1953 and the Designs Act 1953.

The Intellectual Property Office covers two sites, Document and Information Service Centre (DISC) in Seaview and Intellectual Property Office (IPONZ) in Lower Hutt.

The DISC site provides inward and outward mail management, lodgement and cashiering functions, operational processes for the registers and records storage facility for IPONZ.

This Business Continuity Plan has been developed to ensure an effective response to situations that may arise as a result of Y2K failure and in particular:

- No access to the building or primary site,
- Access to building but no IT,
- Access to building, limited IT,
- Access but no infrastructure,
- No Mail Delivery

The primary objective of this plan is to meet any legal requirements, relating particularly to the date and nature of services provided over the critical period.

The specific objectives of this plan are:

1. Date stamp all incoming mail and secure until processing functions are available.
2. Provide for a rapid return to operational status of critical business functions.
3. Permit an orderly transition to normal operations when the damaged or affected facility is restored.
4. Assign responsibilities for the direction of all phases of the Recovery Operation to ensure appropriate staff are informed of progress during each stage of the Recovery Operation, from the time the primary site and/or functions are unavailable until full restoration or alternatives are fully operational.

This plan documents the procedures to be followed by the Impact Assessment and Recovery Teams.

2. OWNERSHIP

Responsibility and ownership of this plan remains within Document & Information Service Centre. The Manager, Janet Dobbie, will be responsible for ensuring the plan is reviewed and updated on a regular basis.

Area of responsibility	Primary	Alternate
Person responsible for this plan is:	Janet Dobbie Manager, Document and Information	Diane Imus National Manager,

Asp Ser Glu Pro
130

<210> 172
<211> 154
<212> PRT
<213> Pinus radiata

<400> 172

Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser Ser Asp Val Leu Lys
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35 40 45

Val Ala Phe Pro Gly Glu Asn Val Leu [illegible] Glu Ala Glu Ile Phe Ser
50 55 60

Thr Thr Tyr Leu Lys Glu Ala Leu Lys Thr Val Pro Ile Ser Ser Ala
65 70 75 80

Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Arg Trp Leu Thr
85 90 95

Asn Phe Pro Arg Leu Glu Ala Arg Asn [illegible] Asp Leu Phe Gly Asn
100 110

Asp [illegible] Leu Glu [illegible] Lys Lys Glu Lys Leu Leu Glu
115 125

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130 135 140

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<210> 173
<211> 82
<212> PRT
<213> Pinus radiata

<400> 173

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35 40 45

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Thr Thr

<210> 174
<211> 141
<212> PRT
<213> Pinus radiata

<400> 174

Glu Tyr Gly Trp Leu Thr Asn Phe Ser Arg Leu Glu Ala Asn Tyr
1 5 15

Ile Asp Phe Phe Gly Lys Asp Ile [illegible] Val Lys Thr Thr Thr
20 30

Lys Glu [illegible] Glu [illegible] Asn Ile Phe

	Service Centre	Corporate Services
Person responsible for overall management of reponse	Janet Dobbie	Gary Jones or Shirley Herewini
Other management Team Members (and roles)	Shirley Herewini Team Leader Records Gary Jones Team Leader Post Acceptance Sue Whiteman Support Services Theresa King Revenue & Lodgement	
Impact Assessment Team (Also Review Team)	Leader Janet Dobbie Members: Shirley Herewini Gary Jones Sue Whiteman	
Recovery Team:	Leader: Janet Dobbie Members: Shirley Herewini Gary Jones Sue Whiteman	
Other Key Staff: (say 3 of this group)	Tania McConnochie Theresa King Jenny Spaans Margaret Newton Joanne Sexton John Aplin William Rodrigues	
Media Contacts	Janet Dobbie	Diane Imus

Key external Contacts:		
Power	TransAlta	Phone: (04) 568 8800
Gas (not supplied to Toop St)	TransAlta	Phone: (04) 568 8800
Water/Effluent Flooding	Hutt City Council After Hours Emergency Service	Phone: (04) 567 2003
Suppliers	DX Post Haste Couriers	Phone: (04) 473 9510 Phone: (04) 499 2121
Others	ABS (Cleaners)	Eric Reille Phone: (04) 564 3249
	Armourguard Security Monitoring Centre	Phone: (04) 478 1226
	Nedax Security	Phone: (04) 471 2836
	Building Manager Melanie Lambert	Phone: (04) 499 9133 After Hours (04) 934 2552 or (025) 262 3146

Emergency Services:	
Fire	111 or Petone Fire Brigade (04) 568 6857
Ambulance	111 or Wellington Free Ambulance (04) 472 2999
Police	111 or Petone Police Station (04) 568 7333
Poisons Centre	Urgent (03) 474 7000 Non Urgent (03) 479 1200
Occupational Health Centre	OK Health Phone (04) 568 7128
Accident and Medical Centre	Hutt Hospital Phone: (04) 566 6999
Lower Hutt Civil Defence	Brian Toomey or Bill Flemming Phone: (04) 570 6666

His Ser Leu Gln Gln Lys Glu Leu Lys Gln Leu Ser Arg Trp Trp Lys
50 55 60
Asp Ser Gly Phe Ser Gln Leu Thr Phe Thr Arg His Arg His Val Glu
65 70 75 80
Phe Tyr Thr Leu Ala Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala
85 90 95
Phe Arg Leu Gly Phe Ala Lys Thr Cys Tyr Leu Gly Ile Val Leu Asp
100 105 110
Asp Ile Tyr Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr
115 120 125
Ala Ala Ile Lys Arg Trp Asp Pro Ser Ala Arg [illegible] Glu Phe
130 135 140

<210> 175
<211> 162
<212> PRT
<213> Pinus radiata

<400> 175
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35 40 45
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50 55 60
Ser Gly Phe Ser Arg Leu Thr Phe Thr Arg His Arg His Val Glu Phe
65 70 75 80
Tyr Thr Leu Ala Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe
85 90 95
Arg [illegible]
100 105 110
Ile Tyr Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala
115 120 125
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130 135 140
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Glu Arg

<210> 176
<211> 74
<212> PRT
<213> Pinus radiata

<400> 176
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20 25 30
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35 40 45
Arg Ser Lys Phe Ala Tyr Leu Ile Gly Leu Ile Gly Arg Leu Leu Asn
50 55 60
Asp Thr Lys Thr Tyr Gln Ala Glu Arg Gly
65 70

<210> 177
<211> 65

IMPACT ASSESSMENT

DISC has identified the following scenarios that will hinder its ability to provide services.

Scenario Presented	Invoke Plan Decision
No access to Seaview area	No
No building access	Yes
Building access, no utilities	Yes
Building access, no IT	Yes
Building access, no IPOL	Yes
No Mail Delivery	Yes

3.1 No Access to Seaview

In the event that Seaview suffers major infrastructure problems the Impact Assessment Team will:

- Contact staff by phone tree
- Leave recorded phone message on (04) 568 0744 for staff information and (04) 568 0720 for Clients' information.

3.2 No Building Access

In the event the Document & Information Service Centre remains closed the Impact Assessment Team will:

- Contact staff by phone tree.
- Leave recorded phone message on (04) 568 0744 for staff information and (04) 568 0720 for Clients' information.

3.3 Building Access no Utilities

If the building is open but there is no power, water or sewerage the Impact Assessment Team will:

- If staff not present, contact by phone tree.
- If staff already present, consider sending staff home.
- If no power, the leader will contact Manager IT Operations.
- Leave recorded phone message on (04) 568 0744 for staff information and (04) 568 0720 for Clients' information.

3.4 Building Access no IT

If all services are available except IT systems the Impact Assessment Team will:

- Re-assign staff to other work.

3.5 Building Access but no IPOL

If the IPOL system is not available the Impact Assessment Team will:

- Re-assign staff to other work.

<212> PRT
<213> Eucalyptus grandis

<400> 177

```
Leu Leu Gly [illegible] Leu Ala Asp Leu Lys Gly Glu Phe Leu Asn Arg
1               5                   10                  15
Lys Glu Val Pro Glu Asn Cys Arg Arg Leu Val Phe Asp Asn Ala Arg
            20                  25                  30
Ser Ser Gln Leu Phe Cys Met Glu Asn Asp Gly Phe Thr His Ser His
        35                  40                  45
Glu Thr Glu Ile Lys Glu His Val Lys Lys Ile Leu Phe Glu Pro Val
    50                  55                  60
Ala
65
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<210> 178
<211> [illegible]
<212> PRT
<213> Eucalyptus grandis

<400> 178

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1               5                   10                  15
Val Gln Asp Ala Pro Lys Glu Lys Val Ile Glu Ala Val Pro Ser Ala
            20                  25                  30
Met [illegible] Glu Ile [illegible] Lys Ser Val Val [illegible] Lys
        35                  40                  45
Met Pro Ser Tyr Ser Leu Glu Ser Lys Leu Gly Asp Cys Lys Arg Ala
    50                  55                  60
Ala Ala Ile Arg Arg Glu Ala Leu Gln Arg Ile Thr Gly Lys Ser Leu
65                  70                  75                  80
Ser Gly Leu Pro Leu Glu Gly Phe Asp Tyr Glu Ser Ile Leu Gly Gln
                85                  90                  95
Cys Cys Glu Met Pro Val Gly Tyr Val Gln Ile Pro Val Gly Ile Ala
            100                 105                 110
Gly [illegible] Arg Gly [illegible] Val Pro
        115                 120                 125
Thr Glu Glu [illegible] Leu Val Ala Ser Thr Asn Arg Gly Cys Lys Ala Ile
    130                 135                 140
Phe Val Ser Gly Gly Ala Thr Ser Val Leu Leu Arg Asp Gly Met Thr
145                 150                 155                 160
Arg Ala Pro Ile Val Arg Phe Gly Thr Ala Lys Arg Ala Ala Asp Leu
                165                 170                 175
Lys Phe Phe Val Glu Asn Pro Ala Asn Phe Glu Ser Leu Ala Val Ile
            180                 185                 190
Phe Asn Arg Ser Ser Arg Phe Ala Arg Leu Gln Ser Ile Lys Cys Ala
        195                 200                 205
Ile Ala Gly Lys Asn Leu Tyr Met Arg Phe Ser Cys Ser Thr Gly Asp
    210                 215                 220
Ala Met Gly Met Asn Met Val Ser Lys Gly Val Gln Asn Val Leu Asp
225                 230                 235                 240
Phe Leu Gln Ser Asp Phe Pro Asp Met Asp Val Leu Gly Ile Ser Gly
                245                 250                 255
Asn Phe Cys Ala Asp Lys Lys Pro Ala Ala Val Asn Trp Ile Glu Gly
            260                 265                 270
Arg Gly Lys Ser Val Val Cys Glu Ala Thr Ile Lys Gly Asp Val Val
        275                 280                 285
Arg Lys Val Leu Lys Thr Ser Val Glu Glu Leu Asp Met Thr
    290                 295                 300
Leu Lys Asn Leu Thr Gly Ser Ala Met Ala Gly Ala Leu Gly Gly Phe
305                 310                 315                 320
```

3.6 No Mail Delivery

If mail is unable to be delivered NZ Post will store the mail until collection can be organised either by DX Courier or ourselves.

4. PLAN SUMMARY

4.1 Objectives

This plan outlines the steps necessary to determine the ability of the Document and Information Service Centre to provide services to IPONZ and its external clients beyond 1 January 2000.

4.2 Before 24 December 1999

Task	Responsibility	Target Date	Completed
Seek assurances from suppliers for Y2K compliance	Sue Whiteman	31 July 1999	Yes
Test all software and relevant hardware for Y2K compliance	IBB/ITS	31 July 1999	Yes
Discuss with Support Services arrangements for alternative accommodation.	Shirley Herewini	30 September 1999	Yes
Contact key suppliers to obtain and confirm contact names	Shirley Herewini Sue Whiteman	31 October 1999	Yes
Distribute copies of BCP plan to all Staff for home and work	Sue Whiteman	15 November 1999	Yes
Inform Clients and Staff of Holiday Period telephone number on which messages will be left.	Janet Dobbie	1 December 1999	Yes
Arrange necessary stationery for date stamping.	Shirley Herewini	15 December 1999	Yes
Arrange storage for mail and cheques	Shirley Herewini	15 December 1999	Yes
Arrange van to be full of petrol.	Shirley Herewini	24 December 1999	

4.3 After 1 January 2000

Task	Responsibility	Target Date
Check that location is accessible, building secure, power on	Armourguard	12:30 am- Armourguard Security to contact Neville Harris (Diane Imus as backup to Neville).
If no power or access to office	Neville Harris to contact Mike Brosnahan	By Jan 1 1am
BRB testing of IT LAN/WAN systems	Michael Brosnahan Joe Flynn (6am initial check)	Jan 1 6am (initial IT ck) Joe Flynn report to Kathryn McInteer 11am 1 Jan Full BRB test start by 1pm 1 Jan. MB to report to Kathryn McInteer by 3pm

```
Asn Ala His Ala Ser Asn Ile Val Ala Ala Ile Phe Ile Ala Thr Gly
                    325                 330                 335
Gln [illegible] Asn Val Glu Ser [illegible] His [illegible] Lys Ile Thr Met Met
            340                 345                 350
Glu Ala Ile Asn Asp Gly Lys Asp Leu His Val Ser Val Thr Met Pro
        355                 360                 365
Ser Val Glu Val Gly Thr Val Gly Gly Gly Thr Gln Leu Ala Ser Gln
    370                 375                 380
Ser Ala Cys Leu Asn Leu Leu Gly Val Lys Gly Ala Asn Lys Glu Leu
385                 390                 395                 400
Ala Gly Ala Asn Ser Arg Leu Leu Ala Thr Val Val Ser Gly Ala Val
                405                 410                 415
Leu Ala Ala Glu Leu Ser Leu Met Ser Ala Ile Ala Ala Gly Gln Leu
            420                 425                 430
Val Lys Ser His Met Lys Tyr Asn Arg Ser Ser Lys Asp Val Thr Lys
        435                 440                 445
Val Ser Ser
    450

<210> 179
<211> 83
<212> PRT
<213> Eucalyptus grandis

<400> 179
Ser Arg Asn Arg Glu Ala Asp Ala Val Val Pro Leu Ala Leu Ala Ser
1               5                   10                  15
Gln Ser Ala Cys Leu Asn Leu Leu Gly Val Lys Gly Glu Lys Glu Leu
            20                  25                  30
Ala Gly Ala Asn Ser Arg Leu Leu Ala Thr Val Val Ser Gly Ala Val
        35                  40                  45
Leu Ala Ala Glu Leu Ser Leu Met Ser Ala Ile Ala Ala Gly Gln Leu
    50                  55                  60
Val Lys Ser His Met Lys Tyr Asn Arg Ser Ser Lys Asp Val Thr Lys
65                  70                  75                  80
Val Ser Ser

<210> 180
<211> 80
<212> PRT
<213> Eucalyptus grandis

<400> 180
Leu [illegible] Lys Ser Thr Gly Asp Ala Met Gly Met Asn
1               5                   10                  15
Met [illegible] Val [illegible] Leu [illegible] Asp
            20                  25                  30
Phe [illegible] Asp Val Met Gly Ile Ser Gly Asn Phe Cys Ser Asp
        35                  40                  45
Lys Lys Pro Ala Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val
    50                  55                  60
Val Cys Glu Ala Val Ile Lys Gly Asp Val Val Arg Lys Val Leu Lys
65                  70                  75                  80

<210> 181
<211> 81
<212> PRT
<213> Eucalyptus grandis

<400> 181
```

Status of IT applications	Michael Brosnahan to notify only if systems not up. Joe Flynn – REGIS/MVSR Les Currie – OASIS Andrew Wagg – WEB Debbie Monahan – IPO Lawrence Wells – CABS	Testing 1 January start 1pm completed by 3pm (see above) Hamilton server rebooted to test OASIS application by David Cole 1.30pm 1 Jan
Full Office site assessment. Complete checklist from Ministry	Diane Imus (both sites)	Report to Brian Hill by 3pm 1 Jan. Janet Dobbie backup
IT Reboots office servers	Bill Vella	By 8am 5 Jan – refer IT BCP
Testing of Applications and processing and Application sponsor report back to Michael Brosnahan with sign-off	Sponsors: Joe Flynn- MVSR Justin Hygate – REGIS Les Currie- OASIS Andrew Wagg- WEB Debbie Monahan- IPO Lawrence Wells- CABS Office tester: Gary Jones (DISC) Debbie Monahan (IPO)	Jan • 11am-Office tester to application sponser. • 12noon –Appl sponser report to MB. • 2pm MB report to KI
Full Office site assessment; Complete checklist from Ministry 1pm 1 Jan.	Gary Jones (DISC) Debbie Monahan (IPO)	Report to Diane Imus by 1pm Jan. DI to report to Brian Hill by 3:30pm.
Conduct post disaster audit appraisal and document results. Amend plan where necessary	Y2K committee	Within 14 working days of return to normal status
Implement Below Only If Problem Identified		
Check outcome of testing on 1 January 2000 and prepare Recovery Team to mobilise if necessary	Janet Dobbie	After 2nd January 2000
Invoke Telephone tree	Janet Dobbie	4 January 2000
Inform key personnel of situation and invoke appropriate action plans	Impact Assessment Team	4 January 2000
Carry out Plan	IA Team	Until necessary
Monitor situation	IA Team	4 hour intervals
Conduct post disaster audit appraisal and document results. Amend plan where necessary	Recovery Team	Within 14 working days of return to normal status

Ser Ile Lys Cys Ala Ile Ala Gly Lys Asn Leu Tyr Leu Arg Phe Ser
1 5 10 15

Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser Lys Gly Val
20 25 30

Gln Asn Val Met Asp Phe Leu Gln Lys Asp Phe Pro Asp Met Asp Val
35 40 45

5. STAFFING AND SUPPORT

Met Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala Ala Val
50 55 60

Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala Val Ile
65 70 75 80

Lys

The Impact Assessment Team is required to be on call to assess the situation after Computer Services BRB IT have completed testing on 2 January 2000. Leader, Janet Dobbie will be responsible for informing the rest of the Team.

Those on-call on 1 January 2000 need only be contacted for a progress report on the outcome of IT services availability. They will be required to make preparations to return to Wellington if the need arises.

<212> PRT
<213> Pinus radiata

<400> 182

Person	Availability	Date & Time	Back-up Resource
Janet Dobbie	On call		Diane Imus
Sue Whiteman	On call		
Gary Jones	On call		
Shirley Heregini	On call		
Rest of DISC staff	Onsite unless otherwise advised a	5 January 8am	

Gly Lys Ser Val Val Cys Glu Ala Leu Ile Lys Glu Glu Val Val Lys
1 5 10 15

Gln Lys Thr Asn Val Ala Ala Leu Val Glu Leu Asn Met Leu
20 25 30

Lys Lys Phe Asn
35 40 45

Ala His Ala Ser Asn Ile Val Ser Ala Ile Tyr Ile Ala Thr Gly Gln
50 55 60

6. INVOKING THE PLAN

Asp Pro Ala Gln Asn Val Glu Ser Ser Thr Met Met Glu
65 70 75 80

Ala Val Asn Glu Gly Arg Asp Leu His Ile Ser Val Thr Met Pro Ser
85 90 95

6.1 Define Operational Status

Ile Glu Val Gly Thr Val Gly Gly Gly Thr Gln Leu Ala Ser Gln Ser
100 105 110

Ala Cys Leu Asn Leu Leu Gly Val Gly Gly

The Impact Assessment Team are responsible for determining the operational status of DISC and the impact on IPONZ operations.
115 120 125

Gly Ala Asn Ala Arg Leu Leu Ala Thr Ile Val
130 135

On or by 2 January 2000 Janet Dobbie will check:

- Power is OK (Armourguard to report back to Neville).
- Access to IPOL is available - Mike Brosnahan by 4pm 1 Jan
- If IPOL or IT is not available BRB IT will be called to assess the problem and make an assessment call on how to proceed.
- If all IT and IPOL OK – Diane Imus to contact Janet and keep informed.
- If the system is still unavailable at 5.30pm on 4 January 2000, Janet Dobbie will inform Impact Assessment Team and staff using the telephone call tree.

<210> 183
<211> 269
<212> PRT

<400> 183

Met Asp Val Arg Arg Arg Gln Pro Lys Pro Pro Arg Pro Ala Ala Gly
1 5 10 15

Asp Pro Arg Arg Arg Gln Lys Ser Leu Arg Leu Pro Ala Pro Gly Val
20 25 30

As a result the Impact Assessment Team will determine the effects of any problems on

Asp Arg Arg Glu Pro Ser Pro Ser Ser Pro Lys Ala Ser Asp Ala Leu
35 40 45

- Staff
- Resources
- Ability to function, and then

Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr Leu Phe Phe
50 55 60

- Decide on the appropriate courses of action for recovery purposes and mobilise the Recovery Team

Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys Ile Arg Ser
65 70 75 80

- Leader - Notify staff and clients by recorded message on phones.
- Leader - Notify BRB Impact team.

Ser Val Pro Ile Val
85 90 95

Ser Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe Gly Ile Gly
100 105 110

6.2 Implement manual system of date stamping

Phe Val Gln Ser Phe Ile Ser Arg Ala Ser His Asp Ala Trp Asp Val
115 120 125

If a manual system is required the Team will:

Leu Asp Asp Glu Val Ala Val Gly Gly Asp Gly Phe Leu Pro Glu Asp

```
130                 135                 140
Asp Gly Pro Pro Cys Ala Ala Ile Ala Cys Ala Pro Pro Lys Leu Ala
145                 150                 155                 160
Glu Arg Gl[illegible]
                165                 170                 175
Val Val Lys Ser Val Thr Asp Gly Lys Ile Pro Ser Tyr Ser Leu Glu
            180                 185                 190
Ser Met Leu Gly Asp Cys Lys Arg Ala Thr Ser Ile Arg Arg Glu Ala
        195                 200                 205
Leu Gln Arg Met Thr Gly Arg Ser [illegible] Lys Gly Leu Pro Leu Glu Gly
    210                 215                 220
Phe Asp Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly
225                 230                 235                 240
Tyr Val Gln Ile Arg Trp Gly Ser Pro Val Arg Cys Cys Ser Thr Gly
                245                 250                 255
Trp Ser Ile Pro Cys Pro Trp Arg Pro Pro Arg Val Ala
            260                 265

<210> 184
<211> 279
<212> PRT
<213> Eucalyptus grandis

<400> 184
Met Asp Val Ser Arg Arg Pro Ser Lys Pro Ala Ala Ala Ala Gly Ser
 1               5                  10                  15
Ser Leu Asp Ala Lys Ser Lys His Ser Pro Ser Pro [illegible] Lys Tyr Tyr
            20                  25                  30
Ala [illegible] Phe Leu Tyr Leu Val
        35                  40                  45
Asn [illegible] Phe Thr Leu Leu Tyr Tyr Leu Leu
    50                  55                  60
Ser Arg Trp Arg Glu Lys Ile Arg Ser Ala Ser Pro Leu His Val Leu
65                  70                  75                  80
Ser Ala Pro Glu Leu Ala Ala Ile [illegible] Ala Ser Ser Val
                85                  90                  95
Tyr Leu Leu Gly Phe Phe Gly Val Glu Phe Phe Gln Ser Leu Leu Leu
            100                 105                 110
Arg Pro Pro Ser Asp Ile Trp Ala Asp Asp Gly Glu [illegible]
        115                 120                 125
Val Ser Val Val Ala Glu Glu Gly Ala Leu Lys Ala Pro Cys Gly Gln
    130                 135                 140
Ala Leu Asp Glu Glu Thr Lys Lys Leu Glu Phe Asp Pro Val Lys Pro
145                 150                 155                 160
Ala Ala Pro Lys Ala Lys Pro Val Glu Thr Glu Lys Trp Asp Glu Pro
                165                 170                 175
Ile Gly [illegible] Val Ile Ala Ser Val Val Ala
            180                 185                 190
Gly [illegible]
        195                 200                 205
Arg Ala Ala Ala Ile Arg Arg Glu Ala Leu Glu Arg Leu Thr Gly Lys
    210                 215                 220
Ser Leu Ala Gly Leu Pro Leu Glu Gly Leu Asp Tyr Asp Ser Ile Leu
225                 230                 235                 240
Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Val Gln Ile Pro Val Gly
                245                 250                 255
Ile Ala Gly Pro Leu Val Leu Asp Gly Arg Glu Tyr Ser Val Pro Met
            260                 265                 270
Ala Thr Thr Glu Gly Cys Leu
        275
```

1. Decide site to be used.
   Note: The above stationery will already be on site as part of the pre 24 December 1999 preparations.
2. Assign Records personnel to the site to:
   - Date stamp all mail appropriately,
   - Put all mail and cheques in date order and deposit in safe.
3. If in usual building and can work, cashiers will:
   - Date stamp all abstracts and cheques,
   - Write up abstracts for private applicants,
   - Balance and check all abstracts and cheques,
   - All cheques and abstracts in date order and put in safe.

7. RETURN TO NORMAL

The Recovery Team will declare a return to normal situation when:

1. Primary site, the building at 17 Toop Street is usable
2. IT link to Toop Street is working and,
3. IPOL is fully functional at Toop Street.

TEST AND REVIEW

The BCP Review Team will review the plan on a monthly basis to ensure all information continues to be correct.

The plan will be discussed with all staff to ensure:

- All staff know whom to contact if necessary,
- All staff are aware of the tasks expected of them before and after the event,
- That all pre-arrangements have been completed by the dates specified,
- That all contact information is up to date.

In the event this plan has been invoked the Impact Assessment Team will be required to conduct a Post Disaster Appraisal within 14 working days of return to normal. Comments and criticism will be sought from other parties where appropriate to determine what improvements can be made to the plan.

Amendments to the plan will be completed and filed within 5 working days of the review being completed.

<210> 185
<211> 194
<212> PRT
<213> Eucalyptus grandis

<400> 185
Met Asp Val Arg Arg Arg Pro Pro Lys Pro Pro Leu Pro Ser Ala Ala
1 5 10 15
Arg Gly Gly Gly Arg Gly Pro Ala Ser Ser Ser Pro Pro Leu Glu Pro
20 25 30
Pro Lys Ala Ser Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala
Val Phe Phe Thr Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg
Trp [illegible] Thr Leu
65 70 75 80
Pro [illegible]
85 90 95
Leu Gly Phe Phe Gly Ile Asp Phe Val Gln Thr Phe Ile Ala Arg Ala
100 105 110
Ser His Asp Ala Trp Glu Asp Leu Asp Asp Asp Val Asn Arg Gly Phe
115 120 125
Gly Cys Thr Asp Ile Val Ala Pro Leu Pro Lys Ser Gly Asp Pro Ala
130 135 140
Pro Val Ile Ser Ala Leu Ser Ser Ala Glu Asp Glu Glu Ile Val Lys
145 150 155 160
Ser Val Val Asp Gly Thr Ile Pro Ser Tyr Ser Leu Glu Ser Lys Leu
165 170 175
Gly [illegible] Ala Ala Phe Val Arg Arg Glu Ala Leu Gln Arg
180 185 190
Thr [illegible]

<210> 186
<211> 136
<212> PRT
<213> Eucalyptus radiata

<400> 186
Met [illegible] Ser Val Ile Ser Leu Pro Ser Asp Phe [illegible]
1 5 10
Thr Ser Phe Ile Asp Arg Ser Gly Arg Glu Leu Asn Pro [illegible]
20
Thr Ile Pro Asn Val Ala Met His Arg Gln Arg Lys Leu [illegible] Met Thr His
40 45
Ala Ser Met Ser Met Asn Leu Arg Thr Ala Val Ser Asp Asp Ala Val
55 60
Ile Lys Arg Arg Gly Asp Phe [illegible]
65 70 75 80
Ile [illegible] Ser Ser Pro [illegible] Ser Tyr [illegible]
85 90
Ala [illegible] Ile Gly Glu [illegible] Arg Phe Asn [illegible]
100 105 110
Asn Glu Asp Gly Glu Ser Ile Thr Pro Leu Asp Asp Leu [illegible]
115 120 125
Leu Trp Met Val Asp Ser Val Glu
135

<210> 187
<211> 140
<212> PRT

9. COMMUNICATION PLAN

Sue Whiteman will be responsible for ensuring copies of the plan are distributed via e-mail to all staff.

Each staff member will be required to have one paper copy at home.

A further copy will be distributed to all staff on the 22nd December 1999.

Communicating to staff of developments – phone message on a particular number (04 568 0744) that they can ring in. Phone messages will be updated by Janet Dobbie.

Communicating to clients and BRB, MOC – phone message (04 568 0720) to be changed by Janet Dobbie.

Poster on door if the building is not in use.

Media release (if necessary) - to be done by the Ministry Communications Unit ONLY

10. APPENDIX

10.1 Contact Details

Name	Position	Contact Number
Janet Dobbie 138 Cockayne Road Ngaio Wellington	Manager, Document & Information Service Centre	(04) 568 0720 work (04) 479 7539 home 021 362 898 mobile
Gary Jones 28 Exploration Way Whitby	Team Leader Post Acceptance	(04) 568 0726 work (04) 234 1400 home
Shirley Piere Waii 100 Shelly Bay Road Shelly Bay	Team Leader Records	(04) 568 0731 work (04) 380 9026 home 025 409 957 mobile
Sue Whiteman State Highway 1 McKays Crossing, Paekakariki	Support Services Duty Manager for Building	(04) 568 0744 work (04) 292 8018 home 025 411 812 mobile
Diane Innus 385c Karori Road Karori Wellington	National Manager Corporate Services Business & Registries Branch	(04) 470 2514 work (04) 476 3459 home 021 342 634 mobile
Janette Campbell	Support Services Manager IPONZ	(04) 560 1601 work (04) 938 7078 home
Debbie Monahan	Manager IPONZ	(04) 560 1615 work 021 306 098 mobile
Michael Brosnahan	IT Operations, BRB	(09) 913 4221 025 443 702 mobile
Chris McKenzie	BRB IT System Administrator	021 532 689 mobile
Nedax Security	Mark Eden	(04) 471 2836
Armourguard Security	Monitoring Centre	(04) 478 1226
DX Post Haste Couriers		Phone: (04) 473 9510 Phone: (04) 499 2121
ASB Cleaners	Eric Reille	(04) 564 3249

<213> Pinus radiata

<400> 187

Met [illegible] [illegible] Val Phe Ala Val Pro Leu Ser Ser Lys Leu Cys Leu Cys
1 5 10 15
Arg Thr Leu Phe Gly Phe Ser His Glu Leu Lys Ala Ile His Ser Thr
20 25 30
Val Pro Asn Leu Gly Met Cys Arg Gly Gly Lys Ser Ile Ala Pro Ser
35 40 45
Met Ser Met Ser Ser Thr Thr Ser Val Ser Asn Glu Asp Gly Val Pro
50 55 60
Arg Arg Ile Ala Gly His His Ser Asn Leu Trp Asp Asp Asp Ile Ile
65 70 75 80
Ala Ser Leu Ser Thr Ser Tyr Glu Ala [illegible] Ser Tyr Arg Glu [illegible] Ala
85 90 95
Asp Lys Leu Ile Gly Glu Val Lys Asn Ile Phe Asp Leu Met Ser Val
100 105 110
Glu Asp Gly Val Phe Thr Ser Pro Leu Ser Asp Leu His His Arg Leu
115 120 125
Trp Met Val Asp Ser Val Glu Arg Leu Gly Ile Asp
130 135 140

		025 454 162

BRB Corporate Phone Tree (in contact order)

Name	Address	Telephone (non business)
Diane Imus	385C Karori Rd Karori, Wellington	04-476-3459 021-342-634 025 243 3432
Neville Harris	48 Penrose St Lower Hutt	04-566-3460 021-459-158 025 241 8382
Andrew Bridgman	3 Fettes Cres Seatoun Heights	04 388 9704 021 306 722
Adam Feeley	36 Fortification Rd Sorching Bay	04 388 2875 021 333 539
Rodney Grindey	26 Taupo Cres Plimmerton	04 233 9080 025 433 013
Karrina Bach	102 Heke Street Ngaio	(04) 479 7399 025 461 868

<210> 188
<211> 68
<212> PRT
<213> Pinus radiata

<400> 188

Leu Gly Met Pro Arg Arg Trp Lys Phe Ala Arg Pro Ser Met Ser Leu
1 5 10 15
Ser Thr Val Ala Ser Asp Asp Asp Ile Gln Arg Arg Thr Gly Gly Tyr
20 25 30
His Ser Asn Leu Trp Asn Asp Asp Val Ile Gln Phe Leu Ser Thr Pro
35 40 45
Tyr Gly Glu Leu Ala Tyr Arg Glu Arg Ala Glu Arg Leu Ile Asp Glu
50 55 60
Val Arg Asn Ile
65

<210> 189
<211> 99
<212> PRT
<213> Pinus radiata

<400> 189

Asp Asp Ala Val Ile Arg Arg Arg Gly Asp Tyr His Ser Asn Ile Trp
1 5 10 15
Asp Tyr Asp Phe Ile Gln Ser Leu Ser Ala Pro Tyr Gly Glu Pro Ser
20 25 30
Tyr Leu Glu Arg Ala Glu Arg Leu Ile Glu Glu Val Lys Lys Val Phe
35 40 45
Asn Ser Met Ser Glu Glu Asn Gly Glu Leu Ile Thr Pro Leu Asn Asp
50 55 60
Leu Ile Gln Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly Ile
65 70 75 80
Asp Arg His Phe Glu Asn Glu Ile Glu Ser Ala Leu Asp Tyr Val Tyr
85 90 95
Ser Tyr Trp

<210> 190

<211> 88
<212> PRT
<213> Pinus radiata

10.2 Telephone Tree Details

- Leader of Impact Assessment Team will ring the three members of Impact Assessment Team who will in turn telephone their staff informing them of the situation.
- Leader (Janet Dobbie) will record phone messages:
  - For staff on (04) 568 0744
  - For clients on (04) 568 0720 for people to ring and obtain information.
- Leader will inform BRB Impact Assessment Team of situation.

Phe His Gln Ile Leu Asn Gly Leu Ala Arg Lys Leu Pro His Asp Ser

Latest telephone List for DISC staff follows:

Ser Ile Tyr Leu Lys Pro Asn Gln Lys Ile Leu Asn Trp Thr Ala Gly

To access office update message: Clients: (04) 568 0720 / Staff: (04) 568 0744

Will Be Rung By	Name	Team	Home Phone Number	Internal Extension
	Janet Dobbie	Manager	(04) 479 7539	8720
Janet Dobbie	Sue Whiteman	Administration	(04) 292 8018	8744
Janet Dobbie	Gary Jones	Post Acceptance Team Leader	(04) 234 1400	8738
Janet Dobbie	Shirley Herewini	Records Team Leader	(04) 380 9026	8731
Janet Dobbie	Christine Edney	Records Centre Advisor	(04) 970 2365	8745
Gary Jones	Jenny Larkin	Post Acceptance	(04) 526 7897	8734
Gary Jones	Jenny Spaans	Post Acceptance	(04) 569 6814	8728
Gary Jones	Margaret Newton	Post Acceptance	(04) 564 7114	8735
Gary Jones	Maria Niway	Post Acceptance	(04) 938 5658	8721
Gary Jones	Moira Macdonald	Post Acceptance	(04) 564 8969	8737
Gary Jones	Suzette Leitner	Post Acceptance	(04) 526 4098	8743
Gary Jones	Thelma Paranihi	Post Acceptance	(04) 563 7205	8727
Shirley Herewini	Joanne Sexton	Records	(04) 560 3564	8736
Shirley Herewini	John Aplin	Records	(04) 564 8969	8761
Shirley Herewini	Tania McConnochie	Records	(04) 569 9219	8746
Shirley Herewini	William Rodrigues	Records	(04) 938 0569	8760
Sue Whiteman	Lindsay Auger	DISC Records Support	(04) 567 7549	8745
Sue Whiteman	Basil Isaac	Revenue & Lodgements	(04) 567 9235	8723
Sue Whiteman	Theresa King	Revenue & Lodgements	(04) 564 4301	8724
Sue Whiteman	Marie McLellan	Revenue & Lodgements	(04) 589 1420	8725
Bob Sykes	Hanley Hoffmann	Hearings Office	(04) 934 3276 or (04) 904 3276	8739
Janet Dobbie	Bob Sykes	Hearings Office	(04) 528 3003	8750
Bob Sykes	Heather Stansfield	Hearings Office	(04) 567 0705	8751
Janet Dobbie	Cath Jones	Searchlink	(025) 985 362	
Janet Dobbie	Diana Imust	Corporate Office	(04) 476 3459	

Ser Asn Ala Asn Gln Leu Ser Ser Met Gly Phe Ala Phe Ser Ser Gly
20 25 30

Ser Leu ... Lys Leu
35 40 45

To change your Voice Mail greeting from an external number phone (04) 560 1679

- Enter your mailbox number
- Enter your password number

Gly Arg Arg Val Gly Lys Ala Tyr Ala Ser Ala Leu Ser Asp Gln Gly
50 55 60

To record a greeting dial 82.

Glu Tyr ... Pro Pro Thr Pro Leu Leu Asp Thr Ile Asn
65 70 75 80

- For an external greeting press 1 and then 5 to start recording your greeting.
- Press 2 to review your greeting and if you wish to re-record your greeting press 76 which will delete your existing greeting, then press 5 to re-record. Press the # key to stop recording.

Tyr Pro Ile His Met Lys Asn Leu Ser Ile Arg Glu Leu Lys Gln Leu
85 90 95

Ser Asn Glu Leu Arg Ser Asp Ile Ile Phe Glu Val Ser Arg Thr Gly
100 105 110

Gly ~~His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu~~
115 120 125

REPORT ON TESTING

His ~~Tyr Val Phe Asp Ala Pro Glu Asp Lys Ile Leu Trp Asp Val Gly~~
130 135 140

Tested on Thursday 30 September and Sunday 3 October 1999.

His Gln ... Asp Lys Met
145 150 155 160

- Tested Telephone Messaging for staff to advise of scenario's for: No Access to Seaview, No Building Access, Building Access no Utilities, Building Access no IT, Building Access no IPOL. Staff rang in to 568 0744 to receive message of availability. Calls logged on voice mail.

Pro Thr Leu ... Ser
165 170 175

Glu Ser Glu Tyr Asp Cys Phe Gly Ala Gly His Ser Ser Thr Ser Ile
180 185 190

Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Glu Asn
195 200 205

Tested on Monday 4 October 1999.

Asn His Val Ile Ser Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
210 215 220

- Tested No Telephone scenario by placing a sign on door to advise staff of IT availability. No IPOL available. All date stamping done manually, no problems.

Ala Phe Gl...
225 230 235 240

Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Asn Leu
245 250 255

Asp Gly Pro Ile Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Lys
260 265 270

- 30 November 1999: Armourguard given specific instructions for manual locking of Main Entrance and Rear Courtyard door at 12.01am on 1 January 2000. Also instructions for check Electricity Status and ringing result through to Neville Harris before 12.30am on 1 January 2000.

Leu Gln Ser Ser Lys Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly
275 280 285

Val Thr Lys Gln Leu Gly Ala Pro Met His Glu Leu Ala Ala Lys Val
290 295 300

Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Arg Ser Thr Leu Phe
305 310 315 320

Glu Glu Leu

<210> 193
<211> 88
<212> PRT
<213> Eucalyptus grandis

<400> 193
Gly Gly His Leu Ser Ala Ser Leu Gly Val Val Glu Leu Thr Val Ala
1 5 10 15

Leu His Asn Val Phe Asn Ala Pro Glu Asp Lys Ile Val Trp Asp Val
20 25 30

Gly His Gln Thr Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Thr Arg
35 40 45

Met His Thr Ile Arg Lys Thr Ser Gly Leu Ala Gly Phe Pro Lys Arg
50 55 60

Asp Glu Ser Val Tyr Asp Thr Phe Gly Val Gly His Ser Ser Thr Ser
65 70 75 80

Ile Ser Ala Gly Leu Gly Met Ala
85

<210> 194

<211> 97
<212> PRT
<213> Eucalyptus grandis

<400> 194
Pro Val Arg Glu Lys Leu Val Lys Ala Trp Arg Asn Asp Ser Glu Ile
1 5 10 15
Phe Ala His Tyr Gly Arg Leu Thr Thr Pro Tyr Ser Asp Glu Leu Leu
20 25 30
Gly Ser Lys Phe Cys Leu His Val Lys Gly Phe Glu Val Asn Thr Ala
35 40 45
Arg Ile Ala Asp Ser Leu Tyr Tyr Gly Cys Val Pro Val Ile Ile Ala
50 55 60
Asn His Tyr Asp Leu Pro Phe Ala Asp Ile Leu Asn Trp Lys Ser Phe
65 70 75 80
Ser Val Val Val Ala Thr Leu Asp Ile Pro Leu Leu Lys Arg Ile Leu
85 90 95
Lys

<210> 195
<211> 149
<212> PRT
<213> Eucalyptus grandis

<400> 195
Gly Met His Thr Ser Lys Phe Cys Leu Asn Pro Ala Gly Asp Thr Pro
1 5 10 15
Ser Ala Cys Arg Leu Phe Asp Ala Ile Val Ser Leu Cys Ile Pro Val
20 25 30
Ile Val Ser Asp Ser Ile Glu Leu Pro Phe Glu Asp Val Ile Asp Tyr
35 40 45
Arg Lys Ile Ala Ile Phe Val Asp Thr Ala Thr Ser Leu Lys Arg Gly
50 55 60
Phe Leu Val Lys Leu Leu Arg Lys Val Arg Thr Glu Lys Ile Leu Glu
65 70 75 80
Tyr Gln Lys Glu Leu Lys Glu Val Lys Arg Phe Phe Glu Tyr Gly Asp
85 90 95
Pro Asn Gly Thr Val Lys Glu Ile Trp Arg Gln Ile Ser Gln Lys Leu
100 105 110
Pro Leu Ile Lys Leu Met Ile Asn Arg Asp Lys Arg Ile Val Lys Arg
115 120 125
Asp Met Ser Glu Pro Asp Cys Ser Cys Ile Cys Ser Asn Gln Thr Gly
130 135 140
Val Ile Ser Thr Leu
145

<210> 196
<211> 196
<212> PRT
<213> Eucalyptus grandis

<400> 196
Met Ser Gln Val Ser Ala Thr Pro Cys Ala Pro Pro Asn Lys Glu Thr
1 5 10 15
Gly His Val Ile Glu Arg Arg Ser Ala Gly Tyr His Pro Ser Val Trp
20 25 30
Gly Asp Tyr Phe Leu Lys Tyr Asp Ser Pro Ser Asn Ser Val Lys Phe
35 40 45
Lys Phe Leu Gly Arg Val Glu Gly Gln Ile Glu Glu Leu Lys Gly Glu
50 55 60

```
Val Lys Lys Met Leu Ile Asp Val Val Asp Lys Pro Leu Pro Lys Leu
65                  70                  75                  80
His Leu Ile Asp Gln Ile Gln Arg Leu Gly Ile Glu Tyr His Phe Glu
                85                  90                  95
Arg Glu Val Asp Glu Gln Leu Glu Gln Ile His Lys Ser Tyr Ser Arg
            100                 105                 110
Leu Asp His Glu Asp Phe Lys Val Asp Asp Leu His Thr Val Ala Leu
        115                 120                 125
Ile Phe Arg Leu Leu Arg Gln His Gly Tyr Asn Ile Ser Ser Glu Ile
    130                 135                 140
Phe Asp Lys Phe Lys Asp Ser Asn Gly Asn Phe Arg Glu Ser Leu Ile
145                 150                 155                 160
Ser Asp Val Arg Gly Leu Leu Ser Leu Tyr Glu Ala Cys His Leu Arg
                165                 170                 175
Cys His Gly Asp Ser Ile Leu Asp Glu Ala Leu Pro Phe Ala Thr Thr
            180                 185                 190
His Leu Glu Ser
        195

      <210> 197
      <211> 116
      <212> PRT
      <213> Eucalyptus grandis

      <400> 197
Met Ser Gln Val Ser Ala Thr Pro Cys Ala Pro Ser Asn Lys Gly Thr
 1               5                  10                  15
Gly His Val Ile Glu Arg Arg Ser Ala Gly Tyr His Pro Ser Val Trp
            20                  25                  30
Gly Asp Tyr Phe Leu Lys Tyr Asp Ser Pro Ser Asn Ser Val Lys Phe
        35                  40                  45
Lys Phe Leu Gly Arg Val Glu Gly Gln Ile Glu Glu Leu Lys Gly Glu
    50                  55                  60
Val Lys Lys Met Leu Thr Asp Ile Met Asp Lys Pro Leu Gln Lys Leu
65                  70                  75                  80
His Leu Ile Asp Gln Ile Gln Arg Leu Gly Ile Glu Tyr His Phe Glu
                85                  90                  95
Arg Glu Ile Asp Glu Gln Leu Glu Gln Ile His Lys Ser Tyr Ser Arg
            100                 105                 110
Leu Asp His Glu
        115

      <210> 198
      <211> 102
      <212> PRT
      <213> Eucalyptus grandis

      <400> 198
Met Ser Leu Pro Ile Ser Arg Val Pro Ser Ser Ser Pro Ala Glu Lys
 1               5                  10                  15
Thr Ser Leu Val Pro Glu Gly Gly Ser Ala Ile Phe His Pro Thr Ile
            20                  25                  30
Trp Ala Asp Tyr Phe Leu Lys His Ala Ser Asn Ser Asn Ser Thr Ser
        35                  40                  45
Ser Asp Gly Val Val Glu Glu His Ile Glu Arg Leu Lys Gly Glu Val
    50                  55                  60
Arg Lys Met Leu Met Gly Ala Met Asp Lys Pro Ser Gln Lys Leu Asn
65                  70                  75                  80
Leu Ile Asp Gln Ile Gln Arg Leu Gly Phe Ala Tyr His Phe Glu His
                85                  90                  95
Glu Ile Asp Glu Gln Leu
```

100

<210> 199
<211> 169
<212> PRT
<213> Eucalyptus grandis

<400> 199
Thr Ser Phe Leu Pro Ser Ser Ile His His Asn Gln Pro Ser Leu Leu
1 5 10 15
Phe Phe Arg His Leu Cys Ser Ser Ser Ser Ala Ala Thr Ser Ser Thr
20 25 30
Ser Ser Gly Ala Gln Phe Val Thr Cys Thr Leu Lys Ile Glu Ala Gln
35 40 45
Glu Ile Gly Arg Arg Ser Ala Asn Trp Gln Pro Asn Val Phe Asp Tyr
50 55 60
Asp Phe Leu Gln Ser Leu Asn Val Asp Tyr Thr Glu Asp Lys Tyr Ser
65 70 75 80
Glu Glu Ala Gln Arg Leu Lys Lys Glu Val Lys Gly Leu Phe Asp Lys
85 90 95
Lys Met Asn Ser Val Ala Lys Leu Glu Phe Ile Asp Val Val Gln Arg
100 105 110
Leu Gly Leu Gly Tyr Gln Phe Glu Thr Glu Ile Lys Asn Ala Leu Ser
115 120 125
Ser Ile Tyr Asn Asn Ala Glu Asp Ala Gln Leu Leu Asp Asp Leu Tyr
130 135 140
Ala Val Ser Leu Arg Phe Arg Leu Leu Arg Gln His Gly Phe Asn Ile
145 150 155 160
Ser Gln Asp Ala Phe Gln Arg Phe Met
165

<210> 200
<211> 132
<212> PRT
<213> Eucalyptus grandis

<400> 200
Ser Ile Arg Pro Asn Gln Pro Ser Leu Ser Leu Phe Ser Arg Pro Arg
1 5 10 15
Ser Ser Phe Ser Ser Pro Ser Ala Val Ser Ser Gly Thr Arg Phe Ala
20 25 30
Lys Cys Ala Leu Thr Ile Glu Asp Glu Asp Thr Ala Arg Arg Ser Ala
35 40 45
Asn Trp Lys Pro Ser Val Trp Asp Tyr Gly Phe Val Gln Ser Leu Asn
50 55 60
Thr Asp Phe Pro Val Asp Lys Tyr Thr Glu Gln Val Gln Arg Leu Lys
65 70 75 80
Glu Glu Val Lys Gly Leu Phe His Arg Glu Met Asn Gln Val Ala Lys
85 90 95
Leu Glu Phe Ile Asp Val Val Gln Arg Leu Gly Leu Gly Tyr His Phe
100 105 110
Glu Thr Glu Ile Asn Asn Ser Leu Ser Ser Ile Tyr Asn Asn Thr Glu
115 120 125
Asp Val Gln Leu
130

<210> 201
<211> 116
<212> PRT
<213> Pinus radiata

<400> 201

Met Ala Ser Val Ser Val Lys Ala Gly Ala Thr Ser Thr Val Ser Cys
1 5 10 15
Gly Leu Ala Ser Asn Asn Leu Ile Arg Arg Thr Ala Asn Pro His Pro
20 25 30
Asn Val Trp Asp Tyr Asp Phe Val His Ser Leu Lys Ser Pro Tyr Asn
35 40 45
Asp Ser Ser Tyr Thr Glu Arg Ala Glu Thr Leu Ile Gly Gln Leu Lys
50 55 60
Val Met Leu Ser Ala Ala Ile Gly Gly Gly Glu Ser Met Ile Thr Pro
65 70 75 80
Ser Ala Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ser Ile Asp Gly
85 90 95
Ser Ala Cys Pro Gln Phe Pro Gln Thr Val Glu Trp Ile Leu Lys Asn
100 105 110
Gln Leu Lys Asp
115

<210> 202
<211> 121
<212> PRT
<213> Pinus radiata

<400> 202

Ala Ile Leu Ser Tyr Pro Pro Glu Ile Leu Ala Leu Pro Ser Pro Ser
1 5 10 15
Phe Leu Tyr Ile Ser Ser Leu Ile Pro Met Ala Ser Val Val Asp Gln
20 25 30
Ala Glu Leu Cys Ser Lys Ser Val Ser Met Ser Ser Pro Gly Val Gln
35 40 45
Arg Arg Thr Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Glu Phe Ile
50 55 60
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
65 70 75 80
Asp Arg Leu Val Gly Glu Val Lys Glu Met Phe Asn Ser Leu Thr Val
85 90 95
Leu Thr Pro His Asn Asp Leu Leu Glu Gln Leu Trp Met Val Asp Ser
100 105 110
Val Glu Arg Leu Gly Ile Asp Arg His
115 120

<210> 203
<211> 259
<212> PRT
<213> Pinus radiata

<400> 203

Asn Ile Gly Pro Ser Phe Leu Ser Ile Ser Ser Leu Val Arg Met Ala
1 5 10 15
Ser Val Val Asp Gln Ala Glu Leu Cys Ser Lys Ser Val Ser Met Ser
20 25 30
Ser Pro Gly Val Gln Arg Arg Thr Gly Asp Tyr His Ser Asn Leu Trp
35 40 45
Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser
50 55 60
Tyr Arg Glu Arg Ala Asp Arg Leu Val Gly Glu Val Lys Glu Met Phe
65 70 75 80
Asn Ser Leu Thr Leu Leu Thr Pro Leu Asn Asp Leu Leu Gln Arg Leu
85 90 95
Trp Met Val Asp Thr Val Glu Arg Leu Glu Ile Asp Arg His Phe Arg
100 105 110

```
Asn Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Ser Glu
        115                 120                 125
Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser
    130                 135                 140
Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Phe Pro Val Ser
145                 150                 155                 160
Ser Asp Val Leu Glu Val Phe Lys Asp Gln Asn Gly Lys Phe Ala Gly
                165                 170                 175
Cys Ser Ala Asn Ala Glu Thr Glu Ala Glu Met Arg Asp Ile Leu Asn
            180                 185                 190
Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu
        195                 200                 205
Glu Ala Gln Thr Phe Cys Thr Ser Tyr Leu Gln Glu Ala Leu Lys Thr
    210                 215                 220
Val Pro Ile Ser Asn Asp Ser Leu Ser Arg Glu Ile Glu Tyr Val Ile
225                 230                 235                 240
Glu Tyr Gly Trp Leu Thr Asn Phe Ser Glu Ile Gly Ser Lys Glu Leu
                245                 250                 255
His Arg Arg
```

<210> 204
<211> 344
<212> PRT
<213> Pinus radiata

<400> 204

```
Ile Asp Val Phe Gly Glu Asp Thr Thr Phe Glu Thr Pro Tyr Leu Ile
1               5                   10                  15
Arg Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His
            20                  25                  30
Ser Leu Val Lys Arg Glu Leu Gln Ser Leu Leu Arg Trp Trp Lys Asp
        35                  40                  45
Tyr Gly Phe Pro Glu Ile Thr Phe Ser Arg His Arg His Val Glu Tyr
    50                  55                  60
Tyr Thr Leu Ala Ala Cys Ile Ala Asn Asp Pro Lys His Ser Ala Phe
65                  70                  75                  80
Arg Leu Gly Phe Gly Lys Ile Ser His Met Ile Thr Ile Leu Asp Asp
                85                  90                  95
Ile Tyr Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Leu Thr Ala
            100                 105                 110
Ala Phe Lys Arg Trp Asp Pro Ser Ser Ile Glu Cys Leu Pro Asp Tyr
        115                 120                 125
Met Lys Gly Val Tyr Met Ala Val Tyr Asp Asn Ile Asn Glu Met Ala
    130                 135                 140
Arg Glu Ala Gln Lys Ile Gln Gly Trp Asp Thr Val Ser Tyr Ala Arg
145                 150                 155                 160
Lys Ser Trp Glu Ala Phe Ile Gly Ala Tyr Ile Gln Glu Ala Lys Trp
                165                 170                 175
Ile Ser Ser Gly Tyr Leu Pro Thr Phe Asp Glu Tyr Leu Glu Asn Gly
            180                 185                 190
Lys Val Ser Phe Gly Ser Arg Ile Thr Thr Leu Glu Pro Met Leu Thr
        195                 200                 205
Leu Gly Phe Pro Leu Pro Pro Arg Ile Leu Gln Glu Ile Asp Phe Pro
    210                 215                 220
Pro Lys Phe Asn Asp Leu Ile Cys Ala Ile Leu Arg Leu Lys Gly Asp
225                 230                 235                 240
Thr Gln Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala
                245                 250                 255
Val Ser Cys Tyr Met Lys Asp His Pro Gly Ile Thr Glu Glu Asp Ala
            260                 265                 270
```

Val Asn Gln Val Asn Ala Met Val Asp Asn Leu Thr Lys Glu Leu Asn
275 280 285
Trp Glu Leu Leu Arg Pro Asp Ser Gly Val Pro Ile Ser Tyr Lys Lys
290 295 300
Val Ala Phe Asp Ile Cys Arg Val Phe His Tyr Gly Tyr Lys Tyr Arg
305 310 315 320
Asp Gly Phe Ser Val Ala Ser Ile Glu Ile Lys Asn Leu Val Thr Arg
325 330 335
Thr Val Val Glu Thr Val Pro Leu
340

<210> 205
<211> 462
<212> PRT
<213> Pinus radiata

<400> 205
Arg Asp Ser Ala Phe Thr Asp Leu Asn Thr Thr Ala Leu Gly Phe Arg
1 5 10 15
Ile Phe Arg Leu His Gly Tyr Thr Val Ser Ser Asp Ala Phe Glu His
20 25 30
Phe Lys Asp Gln Met Gly Gln Phe Ser Ala Ser Ala Asn Asp Thr Glu
35 40 45
Leu Gln Ile Arg Ser Val Phe Asn Leu Phe Arg Ala Ser Leu Ile Ala
50 55 60
Phe Pro Glu Glu Lys Val Leu Glu Glu Ala Glu Asn Phe Ala Ala Ala
65 70 75 80
Tyr Leu Lys Ala Ala Leu Gln Thr Leu Pro Val Ser Gly Leu Ser Arg
85 90 95
Glu Ile Gln Tyr Val Phe Asp Tyr Arg Trp His Ser Asn Leu Pro Arg
100 105 110
Leu Glu Ala Arg Ser Tyr Val Asp Ile Leu Ala Asp Asn Thr Ile Ser
115 120 125
Gly Thr Pro Asp Ala Asn Thr Lys Lys Leu Leu Glu Leu Ala Lys Leu
130 135 140
Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Cys Leu
145 150 155 160
Trp Arg Trp Trp Lys Glu Trp Gly Cys Pro Glu Leu Thr Phe Val Arg
165 170 175
His Arg Tyr Val Glu Phe Tyr Thr Leu Val Ser Gly Thr Asp Met Val
180 185 190
Pro Glu His Ala Ala Phe Arg Leu Ser Phe Val Lys Thr Cys His Leu
195 200 205
Ile Thr Ile Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Ile Asp Glu
210 215 220
Leu Arg Leu Phe Thr Ala Ala Val Lys Arg Trp Asp Pro Ser Ala Thr
225 230 235 240
Glu Cys Leu Pro Glu Tyr Met Lys Gly Val Tyr Arg Val Leu Tyr Glu
245 250 255
Thr Val Asn Glu Met Ala Lys Glu Ala Gln Lys Ser Gln Gly Arg Asp
260 265 270
Thr Leu Gly Tyr Val Arg Gln Ala Leu Glu Asp Tyr Ile Gly Ser Tyr
275 280 285
Leu Lys Glu Ala Glu Trp Ile Ala Thr Gly Tyr Val Pro Thr Phe Gln
290 295 300
Glu Tyr Phe Glu Asn Gly Lys Leu Ser Ser Gly His Arg Ile Ala Thr
305 310 315 320
Leu Gln Pro Ile Leu Thr Leu Ser Ile Pro Phe Pro His His Ile Leu
325 330 335
Gln Glu Ile Asp Phe Pro Ser Lys Phe Asn Asp Tyr Ala Cys Ser Ile
340 345 350

```
Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Ser Ala Arg
        355                 360                 365
Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys Glu Asn Pro Gly
    370                 375                 380
Ser Thr Gln Glu Asp Ala Leu His His Ile Asn Gly Met Ile Glu Asp
385                 390                 395                 400
Met Ile Lys Lys Leu Asn Trp Glu Phe Leu Lys Pro Asp Asn Asn Ala
                405                 410                 415
Pro Ile Ser Ser Lys Lys Asn Ala Phe Asn Ile Ser Arg Gly Leu His
            420                 425                 430
His Phe Tyr Asn Tyr Arg Asp Gly Tyr Ser Val Ala Ser Asn Glu Thr
        435                 440                 445
Lys Asp Leu Val Ile Lys Thr Val Leu Glu Pro Val Leu Met
    450                 455                 460

      <210> 206
      <211> 100
      <212> PRT
      <213> Eucalyptus grandis

      <400> 206
Gly Ser Gln Leu Trp Asp Thr Ala Phe Ala Thr Gln Ala Ile Ile Ser
 1               5                  10                  15
Thr Asn Leu Ile Glu Glu Phe Gly Ser Thr Leu Gln Lys Ala His Thr
            20                  25                  30
Tyr Ile Lys Asn Ser Gln Val Leu Glu Asp Cys Pro Gly Asp Leu Asn
        35                  40                  45
Phe Trp Tyr Arg His Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala
    50                  55                  60
Asp His Gly Trp Pro Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala
65                  70                  75                  80
Ala Leu Val Leu Ser Lys Ile Pro Leu Glu Ile Val Gly Gln Pro Phe
                85                  90                  95
Arg Ser Tyr Gly
            100

      <210> 207
      <211> 89
      <212> PRT
      <213> Eucalyptus grandis

      <400> 207
Met Trp Lys Leu Lys Val Ala Glu Gly Ala Asn Pro Trp Leu Arg Ser
 1               5                  10                  15
Leu Asn Asn His Val Gly Arg Gln Ile Trp Glu Phe Asp Pro Asn Cys
            20                  25                  30
Gly Ser Pro Glu Glu Ile Gln Glu Ile Glu Glu Ala Arg Ala Asn Phe
        35                  40                  45
Leu Lys His Arg Phe Glu Lys Lys His Ser Ser Asp Leu Met Met Arg
    50                  55                  60
Ile Gln Phe Ser Lys Glu Asn Thr Gly Arg Val Val Leu Pro Pro Val
65                  70                  75                  80
Lys Val Lys Asp Leu Asp Glu Ile Thr
                85

      <210> 208
      <211> 198
      <212> PRT
      <213> Eucalyptus grandis

      <400> 208
```

Val Thr His Met Leu Arg Arg Ala Ile Ser Phe His Ser Thr Leu Gln
1 5 10 15
Ala His Asp Gly His Trp Pro Gly Asp Tyr Gly Gly Pro Met Phe Leu
20 25 30
Met Pro Gly Leu Val Ile Ala Leu Ser Ile Thr Gly Ala Leu Asn Ala
35 40 45
Val Leu Ser Glu Gln His Lys Gln Glu Met Cys Arg Tyr Leu Tyr Asn
50 55 60
His Gln Asn Lys Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro Ser
65 70 75 80
Thr Met Phe Gly Ser Val Leu Asn Tyr Val Thr Leu Arg Leu Leu Gly
85 90 95
Glu Ala Ala Asn Asp Gly Gln Gly Ala Met Glu Lys Ala Arg Lys Trp
100 105 110
Ile Leu Asp His Gly Ser Ala Thr Ala Ile Thr Ser Trp Gly Lys Met
115 120 125
Trp Leu Ser Val Leu Gly Ala Phe Glu Trp Ser Gly Asn Asn Pro Leu
130 135 140
Pro Pro Glu Ile Trp Leu Leu Pro Tyr Met Leu Pro Ile His Pro Gly
145 150 155 160
Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu
165 170 175
Tyr Gly Lys Arg Phe Val Ser Pro Ile Thr Pro Thr Val Phe Val Leu
180 185 190
Glu Lys Arg Asn Phe Met
195

<210> 209
<211> 78
<212> PRT
<213> Eucalyptus grandis

<400> 209
Met Trp Lys Leu Lys Ile Ala Glu Gly Gly Pro Trp Leu Thr Ser Val
1 5 10 15
Asn Asn His Val Gly Arg Gln His Trp Glu Phe Asp Pro Asp Ala Gly
20 25 30
Thr Pro Glu Glu Arg Ala Glu Val Glu Arg Val Arg Asp Glu Phe Thr
35 40 45
Arg Asn Arg Phe Arg Ile Lys Gln Ser Ala Asp Leu Leu Met Arg Met
50 55 60
Gln Leu Thr Lys Glu Asn Pro Ser Gly Pro Ile His Arg Arg
65 70 75

<210> 210
<211> 97
<212> PRT
<213> Eucalyptus grandis

<400> 210
Tyr Val Trp Val Gly Glu Asp Gly Ile Lys Met Gln Ser Phe Gly Ser
1 5 10 15
Gln Ile Trp Asp Cys Gly Leu Ser Leu Gln Ala Leu Leu Ala Ser Asp
20 25 30
Leu Ile Asp Glu Ile Gly Pro Val Leu Lys Lys Gly His Glu Phe Leu
35 40 45
Lys Glu Ser Gln Ile Asp Arg Asn Pro Ser Gly Asp Leu Lys Lys Met
50 55 60
Tyr Arg His Ile Ser Lys Gly Ala Trp Ala Phe Ser Asp Lys Asp His
65 70 75 80
Gly Trp Gln Val Ser Asp Cys Thr Ala Glu Ser Met Lys Cys Cys Leu

```
                    85                  90                  95
Val


      <210> 211
      <211> 158
      <212> PRT
      <213> Eucalyptus grandis

      <400> 211
Met Asp Thr Asp Asn Lys Leu Phe Asn Val Gly Val Leu Leu Val Ala
 1               5                  10                  15
Thr Leu Val Val Ala Lys Leu Ile Ser Ala Leu Leu Ile Pro Arg Ser
            20                  25                  30
Gly Lys Arg Leu Pro Pro Val Val Arg Thr Trp Pro Val Val Gly Gly
        35                  40                  45
Leu Leu Arg Phe Leu Lys Gly Pro Met Val Met Leu Arg Glu Glu Tyr
    50                  55                  60
Pro Lys Leu Gly Ser Val Phe Thr Leu Asn Leu Leu Asn Lys Lys Ile
65                  70                  75                  80
Thr Phe Phe Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser
                85                  90                  95
Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr
            100                 105                 110
Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Thr Ile Arg Gln Glu
        115                 120                 125
Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Ile Asn Lys Leu Lys Gly
    130                 135                 140
Tyr Val Asn Gln Met Val Met Glu Ala Glu Asp Tyr Phe Ser
145                 150                 155

      <210> 212
      <211> 131
      <212> PRT
      <213> Eucalyptus grandis

      <400> 212
Met Asp Thr Asp Asn Lys Leu Phe Asn Val Gly Val Leu Leu Val Ala
 1               5                  10                  15
Thr Leu Val Val Ala Lys Leu Ile Ser Ala Leu Leu Ile Pro Arg Ser
            20                  25                  30
Gly Lys Arg Leu Pro Pro Val Val Arg Thr Trp Pro Val Val Gly Gly
        35                  40                  45
Leu Leu Arg Phe Leu Lys Gly Pro Met Val Met Leu Arg Glu Glu Tyr
    50                  55                  60
Pro Lys Leu Gly Ser Val Phe Thr Leu Asn Leu Leu Asn Lys Lys Ile
65                  70                  75                  80
Thr Phe Phe Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser
                85                  90                  95
Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr
            100                 105                 110
Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Thr Ile Arg Gln Glu
        115                 120                 125
Gln Phe Arg
    130

      <210> 213
      <211> 112
      <212> PRT
      <213> Eucalyptus grandis
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<400> 213
Met Asp Thr Asp Asn Lys Leu Phe Asn Val Gly Val Leu Leu Val Ala
1 5 10 15
Thr Leu Val Val Ala Lys Leu Ile Ser Ala Ser Ile Pro Arg Ser Gly
20 25 30
Lys Arg Leu Pro Pro Val Val Arg Thr Trp Pro Val Val Gly Gly Leu
35 40 45
Leu Arg Phe Leu Lys Gly Pro Met Val Met Leu Arg Glu Glu Tyr Pro
50 55 60
Lys Leu Gly Ser Val Phe Thr Leu Asn Leu Leu Asn Lys Lys Ile Thr
65 70 75 80
Phe Phe Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser Glu
85 90 95
Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr Phe
100 105 110

<210> 214
<211> 152
<212> PRT
<213> Eucalyptus grandis

<400> 214
Phe Leu Lys Gly Pro Met Val Met Leu Arg Glu Glu Tyr Pro Lys Leu
1 5 10 15
Gly Ser Val Phe Thr Leu Asn Leu Leu Asn Lys Lys Ile Thr Phe Phe
20 25 30
Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser Glu Ser Asp
35 40 45
Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr Phe Gly Pro
50 55 60
Gly Val Val Phe Asp Val Asp Tyr Thr Ile Arg Gln Glu Gln Phe Arg
65 70 75 80
Phe Phe Thr Glu Ala Leu Arg Ile Asn Lys Leu Lys Gly Tyr Val Asn
85 90 95
Gln Met Val Met Glu Ala Glu Asp Tyr Phe Ser Lys Trp Gly Asp Ser
100 105 110
Gly Glu Val Asp Leu Lys Tyr Glu Leu Glu His Leu Thr Ile Leu Thr
115 120 125
Ala Ser Arg Cys Leu Leu Gly Arg Glu Val Arg Glu Lys Leu Phe Asp
130 135 140
Asp Val Ser Ala Leu Phe His Asp
145 150

<210> 215
<211> 147
<212> PRT
<213> Eucalyptus grandis

<400> 215
Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu Asp Asn Gly Met Leu
1 5 10 15
Pro Ile Ser Val Ile Phe Pro Tyr Leu Pro Ile Pro Ala His His Arg
20 25 30
Arg Asp Lys Ala Arg Lys Lys Leu Ser Glu Ile Phe Ala Asn Ile Ile
35 40 45
Ser Ser Arg Lys Cys Ala Gly Lys Ser Glu Glu Asp Met Leu Gln Cys
50 55 60
Phe Ile Asp Ser Lys Tyr Lys Asn Gly Arg Pro Thr Thr Glu Ala Glu
65 70 75 80
Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala Gly Gln His Thr Ser
85 90 95

Ser Ile Thr Ser Val Trp Thr Gly Ala Tyr Leu Leu Thr Asn Lys Lys
            100   105   110
Tyr Leu Ser Ala Val Ser Asn Glu Gln Lys His Leu Met Glu Lys His
        115   120   125
Gly Asn Asn Val Asp His Asp Val Leu Ser Glu Met Asp Val Leu Tyr
    130   135   140
Arg Ser Ile
145

<210> 216
<211> 129
<212> PRT
<213> Eucalyptus grandis

<400> 216
Tyr Leu Leu Thr Asn Lys Lys Tyr Leu Ser Ala Val Ser Asn Glu Gln
 1   5   10   15
Lys His Leu Met Glu Lys His Gly Asn Asn Val Asp His Asp Val Leu
            20   25   30
Ser Glu Met Asp Val Leu Tyr Arg Ser Ile Lys Glu Ala Leu Arg Leu
        35   40   45
His Pro Pro Leu Ile Met Leu Leu Arg Ser Ser His Ser Asp Phe Ser
    50   55   60
Val Lys Thr Arg Asp Gly Lys Glu Tyr Glu Val Gly Glu Val Ser Val
65   70   75   80
Leu Pro Trp Thr Leu Glu Ala Arg Lys Gly Val Gly Lys Ala Phe Ile
                85   90   95
Thr Ala Phe Arg Ser Gly Ala Val Met Gly Phe Leu Leu Ala Ala Asn
            100   105   110
Gly Leu Leu Val Leu Tyr Ile Ala Ile Asn Leu Phe Lys Ile Tyr Leu
        115   120   125
Trp

<210> 217
<211> 118
<212> PRT
<213> Eucalyptus grandis

<400> 217
Val Val Phe Asp Val Asp Tyr Thr Ile Arg Gln Glu Gln Phe Arg Phe
 1   5   10   15
Phe Thr Glu Ala Leu Arg Ile Asn Lys Leu Lys Gly Tyr Val Asn Gln
            20   25   30
Met Val Met Glu Ala Glu Asp Tyr Phe Ser Lys Trp Gly Asp Ser Gly
        35   40   45
Glu Val Asp Leu Lys Tyr Glu Leu Glu His Leu Thr Ile Leu Thr Ala
    50   55   60
Ser Arg Cys Leu Leu Gly Arg Glu Val Arg Glu Lys Leu Phe Asp Asp
65   70   75   80
Val Ser Ala Leu Phe His Asp Leu Asp Asn Gly Met Leu Pro Ile Ser
                85   90   95
Val Ile Phe Pro Tyr Leu Pro Ile Pro Ala His His Arg Arg Asp Lys
            100   105   110
Ala Arg Lys Lys Leu Ala
        115

<210> 218
<211> 146
<212> PRT
<213> Eucalyptus grandis

<400> 218
Ser Val Arg Arg Arg Ala Leu Glu Met Thr Thr Gly Arg Cys Leu Asp
1 5 10 15
Gly Leu Pro Leu Asp Gly Phe Asp Tyr Gly Ser Ile Leu Gly Gln Cys
20 25 30
Cys Glu Leu Pro Ile Gly Tyr Val Gln Ile Pro Val Gly Val Ala Gly
35 40 45
Pro Leu Leu Leu Asp Gly Ile Glu Asn Met Val Pro Met Ala Thr Thr
50 55 60
Glu Gly Cys Leu Val Ala Ser Thr Asn Arg Gly Cys Lys Ala Ile His
65 70 75 80
Met Ser Gly Gly Ala Thr Ser Val Leu Leu Arg Asp Gly Met Thr Arg
85 90 95
Ala Pro Val Val Arg Phe Pro Thr Ala Arg Arg Ala Ala Gln Leu Lys
100 105 110
Phe Tyr Leu Glu Ala Pro Ile Thr Thr Lys Ala Cys Leu Ser Ser Ser
115 120 125
Thr Ala Pro Ser Lys Val Cys Gln Ala Cys Lys Gly Ile Gln Val Pro
130 135 140
Pro Ile
145

<210> 219
<211> 328
<212> PRT
<213> Eucalyptus grandis

<400> 219
Val Ala Ser Tyr Ser Leu Glu Ser Ala Leu Gly Gly Asp Cys Arg Arg
1 5 10 15
Ala Ala Leu Val Arg Arg Arg Ala Leu Glu Ile Arg Thr Gly Arg Cys
20 25 30
Leu Asp Gly Leu Pro Leu Asp Gly Phe Asp Tyr Gly Ser Ile Leu Gly
35 40 45
Gln Cys Cys Glu Leu Pro Val Gly Tyr Val Gln Ile Pro Val Gly Val
50 55 60
Val Gly Pro Leu Leu Leu Asp Gly Leu Glu Asn Met Val Pro Met Ala
65 70 75 80
Thr Thr Glu Gly Cys Leu Val Ala Ser Ala Asn Arg Gly Cys Lys Ala
85 90 95
Ile His Met Ser Gly Gly Ala Thr Ser Val Leu Leu Arg Asp Gly Met
100 105 110
Thr Arg Ala Pro Val Val Arg Phe Pro Thr Ala Glu Arg Ala Ala His
115 120 125
Leu Lys Ser Tyr Leu Glu His Pro Lys Asn Phe Asp Ser Leu Ser Leu
130 135 140
Ile Phe Asn Ser Thr Ser Arg Phe Ala Arg Leu Gln Thr Ile Lys Cys
145 150 155 160
Ala Ile Ala Gly Arg Asn Leu Tyr Ile Arg Phe Ser Cys Phe Thr Gly
165 170 175
Asp Ala Met Gly Met Asn Met Val Ser Lys Gly Val Gln Asn Val Leu
180 185 190
Asp Phe Leu Gln Asn Glu Asn Pro Asp Met Asp Val Ile Ala Val Ser
195 200 205
Gly Asn Phe Cys Ala Asp Lys Lys Pro Thr Ala Val Asn Trp Ile Glu
210 215 220
Gly Arg Gly Lys Ser Val Val Cys Glu Ala Ile Ile Thr Glu Ala Val
225 230 235 240
Val Ser Lys Val Leu Lys Thr Thr Val Pro Ala Leu Leu Glu Leu Asn
245 250 255

Met Leu Lys Asn Leu Thr Gly Ser Ala Leu Ala Gly Ala Met Gly Gly
260 265 270
Phe Asn Ala His Ala Ser Asn Ile Val Ser Ala Val Phe Ile Ala Thr
275 280 285
Gly Gln Asp Pro Ala Gln Asn Ile Glu Ser Ser His Cys Ile Thr Met
290 295 300
Met Glu Ala Ser Asn Asp Gly Lys Asp Leu His Val Ser Val Thr Met
305 310 315 320
Pro Cys Ile Glu Val Gly Asn Ser
325

<210> 220
<211> 175
<212> PRT
<213> Eucalyptus grandis

<400> 220
Leu Gly Gly Asp Cys Arg Arg Ala Ala Ser Val Arg Arg Arg Ala Leu
1 5 10 15
Glu Met Thr Thr Gly Arg Cys Leu Asp Gly Leu Pro Leu Asp Gly Phe
20 25 30
Asp Tyr Gly Ser Ile Leu Gly Gln Cys Cys Glu Leu Pro Val Gly Tyr
35 40 45
Val Gln Ile Pro Val Gly Val Ala Gly Pro Leu Leu Leu Asp Gly Phe
50 55 60
Glu Ile Met Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser
65 70 75 80
Thr Asn Arg Gly Cys Lys Ala Ile His Met Ser Gly Gly Ala Thr Ser
85 90 95
Val Leu Leu Arg Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ser
100 105 110
Thr Ala Arg Arg Ala Ala Gln Leu Lys Phe Tyr Leu Glu His Pro Asn
115 120 125
Asn Tyr Lys Ser Leu Ser Leu Ile Phe Asn Ser Thr Ser Arg Phe Ala
130 135 140
Arg Leu Gln Gly Ile Lys Cys Ala Ile Ala Gly Arg Asn Leu Tyr Met
145 150 155 160
Arg Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Asp Glu Tyr Gly
165 170 175

<210> 221
<211> 220
<212> PRT
<213> Pinus radiata

<400> 221
Met Glu Ser Cys Gly Ser Gly Ile Ser Gly Thr Gly Lys Lys Met Lys
1 5 10 15
Asn Ser Arg Thr Leu Ala Ser Asp Ala Leu Pro Leu Pro Val Gly Leu
20 25 30
Thr Asn Lys Val Phe Phe Ile Leu Phe Phe Thr Ala Ser Tyr Phe Leu
35 40 45
Met Arg Arg Trp Arg Glu Lys Ile Arg Thr Ser Thr Pro Leu His Val
50 55 60
Leu Ser Leu Gly Glu Leu Val Ala Ile Val Ala Gln Leu Ala Ser Phe
65 70 75 80
Ile Tyr Leu Leu Gly Phe Phe Gly Ile Asp Tyr Val Gln Asn Phe Ile
85 90 95
Thr Gly Gly Asn Asp Asp Asp Asp Ala Arg Glu Asp Asp Lys Leu Arg
100 105 110
Ser Pro Val Pro Lys Glu Ala Val Ala Ile Arg Pro Ser Ala Pro Gln

115 120 125
Val Gln Leu Asn Gly Ile Ser Leu Gly Asp Asn Lys Asp Asp Asp Ile
130 135 140
Ala Ala Ala Val Cys Asn Gly Thr Val Ala Ser Tyr Ser Leu Glu Ser
145 150 155 160
Ser Leu Gly Asp Cys Met Arg Ser Ala Arg Val Arg Arg Arg Ser Leu
165 170 175
Glu Met Met Thr Gly Arg Ser Leu Asp Gly Leu Pro Leu Glu Gly Phe
180 185 190
Asp Tyr Gly Ser Ile Leu Gly Gln Cys Cys Glu Leu Pro Val Gly Tyr
195 200 205
Val Gln Ile Pro Val Gly Val Ala Gly Pro Leu Leu
210 215 220

<210> 222
<211> 91
<212> PRT
<213> Pinus radiata

<400> 222
Asp Leu His Ile Ser Val Thr Met Pro Cys Ile Glu Val Gly Thr Val
1 5 10 15
Gly Gly Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Ile
20 25 30
Gly Val Lys Gly Ala Asn Val Gln Ser Pro Gly Ala Asn Ala Arg Leu
35 40 45
Leu Ala Arg Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu
50 55 60
Met Ser Ala Leu Ala Ala Gly Gln Leu Val Lys Ser His Met Lys Tyr
65 70 75 80
Asn Arg Ser Ile Lys Asp Ile Lys Ala Ile Ser
85 90

<210> 223
<211> 187
<212> PRT
<213> Pinus radiata

<400> 223
Ser Phe Glu Ile His Thr Gly Lys Ser Ala Asp Ile Ser Arg Ala Gln
1 5 10 15
Ser Ala Tyr Thr Gln Gln Asn Asn Asn Ile Phe Thr Ser Ser Lys Ile
20 25 30
His Pro Val Val Ile Val Pro Gly Thr Gly Gly Asn Gln Val Glu Ala
35 40 45
Arg Leu Thr Ala Asp Tyr Lys Pro Ser Gly Leu Leu Cys Arg Arg Trp
50 55 60
Asn Trp Glu Arg Glu Trp Phe Arg Ile Trp Phe Asp Val Pro Val Val
65 70 75 80
Leu Pro Pro Leu Thr Gln Cys Phe Ala Asp Arg Ile Ser Leu Val Tyr
85 90 95
Asp Pro His Thr Asp Glu Tyr Tyr Asn Ala Pro Gly Val Glu Thr Arg
100 105 110
Val Pro Tyr Phe Gly Ser Thr Glu Gly Met Lys Tyr Leu Asp Pro Cys
115 120 125
Phe Lys Tyr Ile Thr Pro Tyr Met Ser Ser Leu Val Lys Ser Leu Glu
130 135 140
Asp Val Gly Tyr Val Asp Gly Lys Ser Leu Phe Gly Ala Pro Tyr Asp
145 150 155 160
Phe Arg Tyr Gly Pro Gly Thr Lys Ser Ser Ser Val Gly Ala Lys Tyr
165 170 175

Leu Glu Asn Leu Arg Lys Leu Val Glu Glu Ala
180 185

<210> 224
<211> 117
<212> PRT
<213> Pinus radiata

<400> 224
Ser Ala Leu Ile Ile Gly Ser Phe Ile Phe Cys Ile Phe Leu Tyr Ile
1 5 10 15
Lys Gly His Val Ala Pro Ser Ser Thr Asp Ser Gly Ser Ser Gly Asn
20 25 30
Val Val Ile Asp Phe Tyr Trp Gly Met Glu Leu Tyr Pro Arg Ile Gly
35 40 45
Lys Asn Phe Asp Ile Lys Val Phe Thr Asn Cys Arg Phe Gly Met Met
50 55 60
Ser Trp Ala Val Leu Ala Val Thr Tyr Ser Ile Lys Gln Tyr Glu Glu
65 70 75 80
Tyr Gly Arg Val Ala Asp Ser Met Leu Val Ser Ser Ile Leu Met Val
85 90 95
Val Tyr Val Thr Lys Val Leu Leu Val Gly Ile Trp Leu Leu Glu His
100 105 110
His Gly Tyr Asn Ser
115

<210> 225
<211> 210
<212> PRT
<213> Pinus radiata

<400> 225
Phe Ala Val Val Gly Pro Leu Gln Leu Thr Ser Tyr Pro Leu Ile Lys
1 5 10 15
Leu Val Gly Ile Arg Thr Gly Leu Pro Leu Pro Ser Leu Trp Glu Ile
20 25 30
Phe Ala Gln Leu Ala Val Tyr Phe Met Val Glu Asp Tyr Gly Asn Tyr
35 40 45
Trp Ile His Arg Trp Leu His Cys Lys Trp Gly Tyr Glu Lys Ile His
50 55 60
His Val His His Glu Phe Thr Ala Pro Met Gly Phe Ala Ala Pro Tyr
65 70 75 80
Ala His Trp Ser Glu Val Leu Ile Leu Gly Ile Pro Thr Phe Val Gly
85 90 95
Pro Ala Ile Ala Pro Gly His Met Ile Thr Phe Trp Cys Trp Val Val
100 105 110
Leu Arg Gln Val Glu Ala Ile Glu Thr His Ser Gly Tyr Asp Phe Pro
115 120 125
Trp Thr Leu Thr Lys Leu Ile Pro Phe Tyr Gly Gly Ala Glu Tyr His
130 135 140
Asp Tyr His His Tyr Val Gly Gly Gln Ser Gln Ser Asn Phe Ala Ser
145 150 155 160
Val Phe Thr Tyr Cys Asp Tyr Leu Tyr Gly Thr Asp Lys Gly Tyr Arg
165 170 175
Tyr Arg Lys Glu His Leu Leu Lys Ala Arg Glu Phe Glu Tyr Arg Leu
180 185 190
Lys Gln Met Ile Leu Arg Lys Lys Thr Ala Met Glu Gln Phe Gln Ile
195 200 205
Ser Leu
210

<210> 226
<211> 86
<212> PRT
<213> Pinus radiata

<400> 226
Gly Pro His Leu Phe Thr Leu Trp Leu Trp Met Ser Leu Arg Val Leu
1   5   10   15
Glu Thr Val Glu Ala His Cys Gly Tyr Asp Phe Pro Trp Ser Ile Ser
            20   25   30
Lys Leu Phe Pro Leu Tyr Gly Gly Ala Asp Phe His Asp Tyr His His
        35   40   45
Arg Leu Leu Tyr Thr Lys Ser Gly Asn Tyr Ser Ser Thr Phe Thr Tyr
    50   55   60
Met Asp Trp Leu Phe Gly Thr Asp Lys Gly Tyr Arg Lys Leu Lys Gly
65   70   75   80
Leu Gln Lys Asp Ser Lys
                85

<210> 227
<211> 141
<212> PRT
<213> Pinus radiata

<400> 227
Met Ala Thr Leu Val Glu Arg Gly Trp Leu Tyr Leu Ile Thr Asn Phe
1   5   10   15
Thr Asp Phe Gln Leu Ala Ser Ile Gly Ser Phe Leu Leu His Glu Ser
            20   25   30
Ile Phe Tyr Leu Ser Gly Leu Pro Phe Ile Leu Leu Glu Thr Thr Gly
        35   40   45
Leu Leu Ser Lys Tyr Lys Ile Gln Ser Lys Thr Asn Thr Val Ala Ala
    50   55   60
Gln Glu Lys Cys Ile Thr Arg Leu Leu Leu Tyr His Phe Cys Val Asn
65   70   75   80
Leu Pro Val Met Val Val Ser Tyr Pro Val Phe Arg Phe Met Gly Met
                85   90   95
Thr Ser Val Leu Pro Leu Pro Ser Trp Lys Val Val Val Ser Gln Leu
            100   105   110
Val Cys Tyr Phe Ile Leu Glu Asp Phe Val Phe Tyr Trp Gly His Arg
        115   120   125
Ile Leu His Ser Lys Trp Leu Tyr Lys His Val His Ser
    130   135   140

<210> 228
<211> 381
<212> PRT
<213> Pinus radiata

<400> 228
Met Gly Glu Glu Leu Gln Thr Trp Ile Leu Met Val Thr Ala Arg Ala
1   5   10   15
Pro Thr Asn Ile Ala Val Ile Lys Tyr Trp Gly Lys Arg Asp Glu Lys
            20   25   30
Leu Ile Leu Pro Ile Asn Asp Ser Ile Ser Phe Thr Leu Asp Pro Asp
        35   40   45
His Leu Ser Ala Thr Thr Thr Val Ala Val Ser Pro Ser Phe Thr Ser
    50   55   60
Asp Arg Met Trp Leu Asn Gly Lys Glu Val Ser Leu Gly Gly Glu Arg
65   70   75   80
Tyr Gln Asn Cys Leu Arg Glu Ile Arg Ser Arg Gly Asn Asp Val Val

```
                85                  90                  95
Asp Glu Lys Lys Gly Ile Val Ile Arg Lys Glu Asp Trp Gln Arg Leu
            100                 105                 110
His Leu His Ile Ala Ser Tyr Asn Asn Phe Pro Thr Ala Ala Gly Leu
        115                 120                 125
Ala Ser Ser Ala Ala Gly Phe Ala Cys Leu Val Tyr Gly Leu Ala Lys
    130                 135                 140
Leu Met Asp Val Lys Glu Lys Tyr Gln Gly Glu Leu Ser Ala Ile Ala
145                 150                 155                 160
Arg Arg Gly Ser Gly Ser Ala Cys Arg Ser Leu Tyr Gly Gly Val Val
                165                 170                 175
Lys Trp Met Met Gly Lys Glu Thr Asp Gly Ser Asp Ser Ile Ala Val
            180                 185                 190
Gln Leu Ala Thr Glu Lys His Trp Glu Asp Leu Val Ile Leu Ile Ala
        195                 200                 205
Val Val Ser Ser Arg Gln Lys Glu Thr Ser Ser Thr Thr Gly Met Ser
    210                 215                 220
Gln Ser Val Glu Thr Ser Glu Leu Leu Arg His Arg Ser Gln Glu Val
225                 230                 235                 240
Val Pro Lys Arg Ile Leu Gln Ile Glu Glu Ala Ile Ala Asn His Asp
                245                 250                 255
Phe Gly Ser Phe Ala Lys Ile Thr Cys Ala Asp Ser Asn Gln Phe His
            260                 265                 270
Ala Val Cys Leu Asp Thr Ser Pro Pro Ile Phe Tyr Met Asn Asp Thr
        275                 280                 285
Ser His Arg Ile Ile Asn Cys Ile Glu Arg Trp Asn Arg Ser Glu Gly
    290                 295                 300
Thr Pro Gln Val Ala Tyr Thr Phe Asp Ala Gly Pro Asn Ala Val Met
305                 310                 315                 320
Tyr Ala Pro Asn Arg Lys Val Ala Gly His Leu Leu Gln Arg Leu Leu
                325                 330                 335
Phe Tyr Phe Pro Pro Asp Ser Ser Lys Thr Leu Ser Ser Tyr Val Ile
            340                 345                 350
Gly Asp Thr Ser Ile Leu Gly Glu Ile Gly Val Asp Ser Met Lys Asp
        355                 360                 365
Val Glu Ser Leu Thr Ala Pro Pro Glu Leu Lys Ser Glu
    370                 375                 380

      <210> 229
      <211> 81
      <212> PRT
      <213> Pinus radiata

      <400> 229
Met Gly Glu Glu Leu Gln Thr Trp Ile Leu Met Val Thr Ala Arg Ala
 1               5                  10                  15
Pro Thr Asn Ile Ala Val Ile Lys Tyr Trp Gly Lys Arg Asp Glu Lys
            20                  25                  30
Leu Ile Leu Pro Ile Asn Asp Ser Ile Ser Phe Thr Leu Asp Pro Asp
        35                  40                  45
His Leu Ser Ala Thr Thr Thr Val Ala Val Ser Pro Ser Phe Thr Ser
    50                  55                  60
Asp Arg Met Trp Leu Asn Gly Lys Glu Val Ser Leu Gly Gly Glu Arg
65                  70                  75                  80
Tyr


      <210> 230
      <211> 189
      <212> PRT
      <213> Pinus radiata
```

<400> 230

Met Pro Leu Thr Leu Leu Leu Ala Asn Thr Trp Ala Ser Ser Ala Ile
1 5 10 15
Val Ser Arg Arg Val Ser Leu Phe Val Ala Cys Ser Thr Thr Val Val
20 25 30
Ser Arg Ser Phe Ser Lys Ser Cys Ser Gly Ala Ile Pro Arg Lys Pro
35 40 45
Lys Ser Ala His Pro Ala Leu Thr Gly Ser Arg Thr Cys Phe Ser Arg
50 55 60
Asn Pro Ile Val Arg Asn Leu Ile Gly Ser Ala Ser Lys Met Gly Ala
65 70 75 80
Thr Val Glu Asp Thr Thr Met Asp Ala Val Gln Arg Arg Leu Met Phe
85 90 95
Glu Asp Glu Cys Ile Leu Val Asp Glu Glu Asp His Val Ile Gly His
100 105 110
Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ser Glu Asn
115 120 125
Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Thr Lys Tyr Glu
130 135 140
Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val
145 150 155 160
Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
165 170 175
Ile Glu Glu Asn Asn Leu Gly Ser Glu Met Gln Pro Lys
180 185

<210> 231
<211> 113
<212> PRT
<213> Pinus radiata

<400> 231

Met Ala Gly Ile Pro Val Leu Arg Pro Phe Cys Ile Cys Leu Leu Ser
1 5 10 15
Val Tyr Met Leu His Ile Val Ala Ala Val Ala Ser Pro Arg Leu Gly
20 25 30
Arg Ser Ser Phe Pro Arg Gly Phe Lys Phe Gly Ala Gly Ser Ser Ala
35 40 45
Tyr Gln Ala Glu Gly Ala Ala His Glu Gly Gly Lys Gly Pro Ser Ile
50 55 60
Trp Asp Thr Phe Ser His Thr Pro Gly Lys Ile Ala Asp Gly Lys Asn
65 70 75 80
Gly Asp Val Ala Val Asp Gln Tyr His Arg Tyr Lys Glu Asp Val Gln
85 90 95
Leu Leu Lys Tyr Met Gly Met Asp Val Tyr Arg Phe Ser Ile Ser Trp
100 105 110
Ser

<210> 232
<211> 127
<212> PRT
<213> Pinus radiata

<400> 232

Gly Pro Ser Ile Trp Asp Thr Phe Ser His Thr Pro Gly Lys Ile Ala
1 5 10 15
Asp Gly Lys Asn Gly Asp Val Ala Val Asp Gln Tyr His Arg Tyr Lys
20 25 30
Glu Asp Val Gln Leu Leu Lys Asn Met Gly Met Asp Val Tyr Arg Phe

35 40 45
Ser Ile Ser Trp Ser Arg Ile Phe Pro Lys Gly Ser Pro Arg His Gly
50 55 60
Pro Val Asn Lys Val Gly Ile Val Tyr Tyr Asn Asn Phe Ile Asn Glu
65 70 75 80
Leu Leu Arg Asn Gly Ile Glu Pro Phe Val Thr Leu Phe His Trp Asp
85 90 95
Met Pro Gln Ala Leu Glu Asp Glu Tyr Gly Gly Phe Arg Asn Lys Arg
100 105 110
Val Val Glu Asp Phe Asn Ile Phe Ala Glu Ala Cys Phe Arg Ala
115 120 125

<210> 233
<211> 118
<212> PRT
<213> Eucalyptus grandis

<400> 233
Met Ala Gly Glu Trp Ile Leu Thr Leu Thr Ala Gln Thr Pro Thr Asn
1 5 10 15
Ile Ala Val Ile Lys Tyr Trp Gly Lys Arg Asp Glu Ser Leu Ile Leu
20 25 30
Pro Val Asn Asp Ser Ile Ser Val Thr Leu Asp Pro Gly His Leu Cys
35 40 45
Thr Thr Thr Thr Val Ala Val Ser Pro Ala Phe Glu Gln Asp Arg Met
50 55 60
Trp Leu Asn Gly Lys Glu Ile Ser Leu Ser Gly Asp Arg Phe Gln Ser
65 70 75 80
Cys Leu Arg Glu Ile Arg Ala Arg Ala Thr Asp Val Glu Asn Lys Glu
85 90 95
Lys Gly Ile Lys Ile Ser Lys Lys Asp Trp Glu Lys Leu His Leu His
100 105 110
Ile Ser Phe Phe Thr Phe
115

<210> 234
<211> 111
<212> PRT
<213> Pinus radiata

<400> 234
Met Met Gln Lys Tyr Ile Gly Ala Asp Val Thr Ser Met Val Thr Leu
1 5 10 15
Pro Val Ile Ile Phe Glu Pro Met Thr Met Leu Gln Lys Ser Ala Glu
20 25 30
Leu Met Glu Tyr Thr Tyr Leu Leu Asp Met Ala Asp Glu Cys Glu Asp
35 40 45
Pro Tyr Leu Lys Met Ala Tyr Ala Ala Ser Trp Ala Ile Ser Val Tyr
50 55 60
Pro Ala Tyr Gln Arg Ser Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu
65 70 75 80
Thr Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ala Glu Gln
85 90 95
Val Ser His His Pro Pro Trp Ala Gln Pro Met Pro Glu Met Thr
100 105 110

<210> 235
<211> 391
<212> PRT
<213> Pinus radiata

<400> 235
Met Met Gln Lys Tyr Ile Gly Ala Asp Val Thr Ser Met Val Thr Leu
1 5 10 15
Pro Val Ile Ile Phe Glu Pro Met Thr Met Leu Gln Lys Ser Ala Glu
20 25 30
Leu Met Glu Tyr Thr Tyr Leu Leu Asp Met Ala Asp Glu Cys Glu Asp
35 40 45
Pro Tyr Leu Lys Met Ala Tyr Ala Ala Ser Trp Ala Ile Ser Val Tyr
50 55 60
Pro Ala Tyr Gln Arg Ser Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu
65 70 75 80
Thr Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ala Glu Gln
85 90 95
Val Ser His His Pro Pro Met Gly Ser Ala Tyr Ala Glu Asn Glu His
100 105 110
Phe Thr Tyr Ser Leu Ser Ser Lys Val Lys Thr Lys Phe Leu Gly Asn
115 120 125
Ser Val Asp Ile Tyr Pro Leu Gly Arg Thr Arg Val Val Leu Lys Lys
130 135 140
Ser Gly Asp Val Leu Asp Leu Val Pro Pro Pro Ser Lys Val His Asn
145 150 155 160
Leu Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Val Leu
165 170 175
Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys
180 185 190
Gly Trp Phe Gly Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asp
195 200 205
Ser Lys Glu Glu Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Arg Ser
210 215 220
Met Gly Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro Leu Pro Gly Thr
225 230 235 240
Glu Leu Lys Glu Val Trp Arg Val Ala Asp Leu Pro Lys Asn Asp Lys
245 250 255
Phe Gln Tyr Thr Tyr Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala
260 265 270
Pro Lys Lys Leu Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Ser
275 280 285
Ala Leu Glu Met Gly Asp Leu Ser Lys Ala Gly Ala Glu Lys Ser Asn
290 295 300
Leu Glu Glu Arg Gln Arg Ala Glu Lys Arg Cys Arg Glu Glu Lys Asn
305 310 315 320
Gln Pro Phe Thr Pro Arg Trp Phe Thr Val Thr Gly Glu Val Ala Thr
325 330 335
Thr Pro Trp Gly Asp Leu Glu Val Tyr Glu Tyr Asn Gly Lys Tyr Ser
340 345 350
Glu His Arg Ala Ser Val Asp Asp Ser Asn Phe Asp Asp Gly Thr Asp
355 360 365
Ser Lys Ser Met Glu Phe Asn Pro Trp Gln Tyr Gly Asn Ile Glu Ser
370 375 380
Gly Ser Asn Lys Lys Val Glu
385 390

<210> 236
<211> 27
<212> PRT
<213> Pinus radiata

<400> 236
Met Met Gln Lys Tyr Ile Gly Ala Asp Val Thr Ser Met Val Thr Leu
1 5 10 15
Pro Val Ile Ile Phe Glu Pro Met Thr Met Leu

20 25

<210> 237
<211> 134
<212> PRT
<213> Pinus radiata

<400> 237
Tyr Leu Val Leu Ile Ser Gln Leu Arg Val Gly Met Asp Leu Ser Lys
1 5 10 15
Val Thr Phe Pro Thr Phe Val Leu Glu Pro Arg Ser Met Leu Glu Arg
20 25 30
Ile Thr Asp Phe Met Ser His Pro Asp Leu Ile Phe Gly Ala Glu Asn
35 40 45
Ser Asn Asp Pro Glu Glu Arg Phe Met Arg Val Leu Ser Tyr Tyr Leu
50 55 60
Ala Gly Trp His Ile Lys Pro Lys Gly Val Lys Lys Pro Tyr Asn Pro
65 70 75 80
Val Leu Gly Glu Phe Phe Arg Cys Arg Tyr Asp Tyr Ser Asn Asn Thr
85 90 95
Gln Gly Phe Tyr Ile Ala Glu Gln Val Ser His His Pro Pro Ile Ser
100 105 110
Ala Phe Phe Tyr Ile Ser Pro Ala Asn Arg Val Ser Ile Ile Gly Glu
115 120 125
Leu Arg Pro Lys Ser Lys
130

<210> 238
<211> 133
<212> PRT
<213> Eucalyptus grandis

<400> 238
Ser Ser Lys Gly Arg His Cys Lys Pro Phe Asn Pro Leu Leu Gly Glu
1 5 10 15
Thr Tyr Glu Ala Asp Tyr Pro Glu Arg Gly Val His Phe Phe Ser Glu
20 25 30
Lys Val Ser His His Pro Thr Leu Ile Ala Cys His Cys Glu Gly Arg
35 40 45
Gly Trp Lys Phe Trp Ala Asp Ser Asn Leu Arg Thr Lys Phe Trp Gly
50 55 60
Gln Ser Ile Gln Leu Asp Pro Val Gly Ala Leu Thr Leu Glu Phe Asp
65 70 75 80
Asp Gly Glu Ile Phe Gln Trp Asn Lys Val Thr Thr Ser Ile Asn Asn
85 90 95
Leu Ile Ile Gly Lys Val Tyr Cys Asp His His Gly Val Met Asn Ile
100 105 110
His Gly Asn His Gln Tyr Ser Cys Lys Leu Lys Phe Lys Glu Pro Ser
115 120 125
Ile Leu Ala Glu Leu
130

<210> 239
<211> 116
<212> PRT
<213> Eucalyptus grandis

<400> 239
Arg Thr Cys Asp Trp Ser Met Arg Ala Ser Trp Ala Ile Ser Val Tyr
1 5 10 15
Tyr Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu

```
            20                        25                       30
Thr Tyr Glu Leu Ala Asn His Gly Gly Ile Thr Phe Ile Ala Glu Gln
        35                      40                      45
Val Cys His His Pro Pro Met Ser Ala Gly His Ala Glu Asn Asp His
    50                      55                      60
Phe Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn
65                      70                      75                      80
Ser Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg
                85                      90                      95
Asp Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys Val Asn Asn
            100                     105                     110
Leu Ile Phe Gly
        115
```

<210> 240
<211> 105
<212> PRT
<213> Eucalyptus grandis

<400> 240

```
Ser Arg Leu Arg Pro Asp Arg Tyr Ala Leu Glu Pro Gly Asp Leu Pro
 1               5                  10                  15
Lys Ala Gly Ala Glu Lys Ser Ser Leu Glu Glu Arg Gln Arg Gly Glu
            20                  25                  30
Lys Lys Asn Arg Glu Met Lys Gly Gln Lys Phe Thr Pro Arg Trp Phe
        35                  40                  45
Asp Leu Thr Asp Glu Ile Ser Pro Thr Pro Trp Gly Asp Leu Glu Val
    50                  55                  60
Tyr Arg Tyr Asn Gly Lys Tyr Thr Glu His Arg Ala Val Val Asp Ser
65                  70                  75                  80
Leu Asp Thr Ile Glu Glu Ser Asp Ile Gln Ser Thr Glu Phe Asn Pro
                85                  90                  95
Trp Gln Tyr Glu Ala Thr Phe Ala Glu
            100                 105
```

<210> 241
<211> 117
<212> PRT
<213> Pinus radiata

<400> 241

```
Val Leu Arg Gly Leu Asp Thr Val Glu Asp Asp Thr Ser Ile Pro Leu
 1               5                  10                  15
Asp Thr Lys Leu Pro Ile Leu Lys Ala Phe Tyr Lys His Ile Tyr Asp
            20                  25                  30
Pro Ser Trp His Phe Ser Cys Gly Val Glu His Tyr Lys Glu Leu Met
        35                  40                  45
Glu Lys Phe His His Val Ser Thr Thr Phe Leu Arg Leu Gly Arg Gly
    50                  55                  60
Tyr Gln Glu Ala Ile Glu Glu Ile Thr Lys Lys Met Gly Ala Gly Met
65                  70                  75                  80
Ala Lys Phe Ile Cys Lys Glu Val Glu Ser Val Glu Asp Tyr Asp Glu
                85                  90                  95
Tyr Cys His Tyr Val Ala Gly Leu Val Gly Phe Gly Leu Ser Arg Leu
            100                 105                 110
Phe His Ala Ala Gln
        115
```

<210> 242
<211> 190
<212> PRT

<213> Pinus radiata

<400> 242
Met Ala Ile Tyr Thr Pro Gln Pro Ala His Arg Leu Ile Ser Trp Ser
1   5   10   15
Thr Met Glu Asn His Thr Val Val Ile Ala Ala Ala Ile Ser Phe Val
            20   25   30
Ser Val Leu Leu Ser Tyr Tyr Ile Val Leu Ser Arg Trp Lys Arg Arg
        35   40   45
Ser Asn Gly Leu Arg Gly Ile Gln Ser Lys Ser Phe Glu Lys Ser Thr
    50   55   60
Asp Asp Asn Gly Ile Ala Ile Glu Ala Ala Gly Gly Thr Asp Val Ile
65   70   75   80
Ile Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly
                85   90   95
Lys Asp Gly Arg Arg Ile His Val Ile Glu Arg Asp Leu Ser Glu Pro
            100   105   110
Asp Arg Ile Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu
        115   120   125
Ile Glu Leu Gly Leu Gln Asp Cys Val Glu Gly Ile Asp Ala Gln Ser
    130   135   140
Ile Phe Gly Asp Ala Leu Phe Lys Glu Gly Lys Asp Thr Lys Val Ala
145   150   155   160
Tyr Pro Leu Glu Asn His His Ala Asp Arg Ala Gly Arg Ser Phe His
                165   170   175
Asn Gly Arg Phe Ile Gln Arg Met Arg Glu Lys Ala Ala Ser
            180   185   190

<210> 243
<211> 124
<212> PRT
<213> Pinus radiata

<400> 243
Cys Leu Thr Thr Asp Ser Gly Gln Val Ile Asn Cys Arg Asn Arg Tyr
1   5   10   15
Thr Ala Met Ala Ile Tyr Thr Pro Gln Pro Ala His Arg Leu Ile Ser
            20   25   30
Trp Ser Thr Met Glu Asn His Thr Val Ala Ile Ala Val Ala Ile Gly
        35   40   45
Phe Val Ser Val Leu Leu Ser Tyr Tyr Ile Val Leu Asn Arg Trp Lys
    50   55   60
Arg Arg Ser Asn Gly Leu Arg Gly Ile Gln Ser Lys Ser Phe Glu Lys
65   70   75   80
Ser Thr Asp Asp Asn Gly Ile Ala Ile Glu Ala Ala Gly Gly Thr Asp
                85   90   95
Val Ile Ile Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr
            100   105   110
Leu Gly Lys Asp Gly Arg Arg Ile His Val Ile Glu
        115   120

<210> 244
<211> 123
<212> PRT
<213> Eucalyptus grandis

<400> 244
Met Asp Gly Gln Tyr Leu Val Ser Gly Val Leu Ala Leu Phe Leu Gly
1   5   10   15
Ile Phe Leu Leu Tyr Lys Gly Leu Gly Lys Gln Lys Arg Arg Leu Ser
            20   25   30

Lys Lys Gly Arg Gly Asp Asp Tyr Val Lys Ser Ser Val Asp Gly Gly
35 40 45
Phe Val Pro Gly Gly Val Asp Gly Ser Thr Asp Ile Val Ile Val Gly
50 55 60
Ala Gly Val Ala Gly Ala Ala Leu Ala Tyr Ala Leu Gly Lys Asp Gly
65 70 75 80
Arg Arg Val Arg Val Ile Glu Arg Asp Leu Thr Glu Gln Asp Arg Ile
85 90 95
Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Met Glu Leu
100 105 110
Asp Leu Ala Asp Cys Val Gln Thr Ile Asp Ala
115 120

<210> 245
<211> 221
<212> PRT
<213> Eucalyptus grandis

<400> 245
Leu Gly Ser Lys Tyr Lys Pro Gln Glu Glu Phe Val Glu Trp Ile Gln
1 5 10 15
Lys Gly Thr Lys Pro Ile Tyr Ile Gly Phe Gly Ser Met Pro Leu Glu
20 25 30
Asp Pro Lys Lys Thr Thr Asp Ile Ile Ile Lys Ala Leu Thr Asp Thr
35 40 45
Gly Gln Arg Gly Ile Val Gly Arg Gly Trp Gly Asp Leu Gly Thr Leu
50 55 60
Leu Asp Val Pro Asp Ser Val Phe Leu Leu Glu Asp Cys Pro His Asp
65 70 75 80
Trp Leu Phe Pro Gln Cys Ser Ala Val Val His His Gly Gly Ala Gly
85 90 95
Thr Thr Ala Thr Gly Leu Lys Ala Gly Cys Pro Thr Thr Ile Val Pro
100 105 110
Phe Phe Gly Asp Gln Phe Phe Trp Gly Asp Arg Val His Gln Arg Gly
115 120 125
Leu Gly Pro Ala Pro Ile Pro Ile Ser Gln Leu Ser Val Glu Asn Leu
130 135 140
Ser Asp Ala Ile Arg Phe Met Leu Gln Pro Glu Val Lys Ser Gln Ala
145 150 155 160
Met Glu Met Ala Lys Leu Ile Glu Asn Glu Asp Gly Val Ala Ala Ala
165 170 175
Val Asp Ala Phe His Arg His Leu Pro Glu Glu Phe Pro Ser Ser Ser
180 185 190
Val Ser Ser Asp Gly Glu Glu His Pro Asn Pro Phe Leu Trp Leu Phe
195 200 205
Leu Gln Val Glu Lys Trp Cys Cys Leu Pro Cys Ser Lys
210 215 220

<210> 246
<211> 114
<212> PRT
<213> Eucalyptus grandis

<400> 246
Leu Asp Asn Cys Pro His Asp Trp Leu Phe Leu Arg Cys Ser Ala Val
1 5 10 15
Val His His Gly Gly Ala Gly Thr Thr Ala Ala Gly Leu Lys Ala Ala
20 25 30
Cys Pro Thr Thr Val Val Pro Phe Phe Gly Asp Gln Pro Phe Trp Gly
35 40 45
Glu Arg Val His Ala Arg Gly Val Gly Pro Val Pro Ile Pro Val Asp

```
    50                  55                  60
Glu Phe Ser Leu Glu Lys Leu Val Asp Ala Ile Arg Phe Met Leu Asp
65                  70                  75                  80
Pro Lys Val Lys Gln Cys Ala Glu Glu Leu Ala Lys Asp Met Glu His
                85                  90                  95
Glu Asp Gly Val Glu Gly Ala Val Lys Ala Phe Tyr Lys His Phe Pro
            100                 105                 110
Arg Glu


      <210> 247
      <211> 140
      <212> PRT
      <213> Pinus radiata

      <400> 247
Met Ala Thr Gly Gly Gly Ala Leu Asp Leu Ala Ser Gly Met Gly Gly
 1               5                  10                  15
Asn Ile Glu Lys Glu Gln Met Leu Thr Ala Val Glu Glu Tyr Glu Lys
            20                  25                  30
Tyr His Met Tyr Tyr Gly Gly Asp Glu Gly Ser Arg Lys Ser Asn Tyr
        35                  40                  45
Thr Asp Met Val Asn Lys Tyr Tyr Asp Leu Ala Thr Ser Phe Tyr Glu
    50                  55                  60
Tyr Gly Trp Gly Glu Ser Phe His Phe Ala His Arg Trp Lys Gly Glu
65                  70                  75                  80
Thr Leu Arg Glu Ser Ile Lys Arg His Glu His Phe Leu Ala Leu His
                85                  90                  95
Leu Cys Leu Lys Pro Ala Met Lys Val Leu Asp Val Gly Cys Gly Ile
            100                 105                 110
Gly Gly Pro Leu Arg Glu Ile Ala Arg Phe Ser Arg Thr Ser Ile Thr
        115                 120                 125
Gly Leu Asn Asn Asn Ala Tyr Gln Ile Ser Arg Gly
    130                 135                 140

      <210> 248
      <211> 152
      <212> PRT
      <213> Eucalyptus grandis

      <400> 248
Met Ser Lys Ala Gly Ala Met Asp Leu Ala Thr Gly Leu Gly Gly Lys
 1               5                  10                  15
Met Asp Lys Ser Asp Val Leu Ser Ala Val Asp Lys Tyr Glu Lys Tyr
            20                  25                  30
His Val Cys Tyr Gly Gly Asp Glu Glu Glu Arg Arg Ala Asn Tyr Ser
        35                  40                  45
Asp Met Val Asn Lys Tyr Tyr Asp Leu Ala Thr Ser Phe Tyr Glu Phe
    50                  55                  60
Gly Trp Gly Glu Ser Phe His Phe Ala His Arg Trp Lys Gly Glu Ser
65                  70                  75                  80
Leu Arg Glu Ser Ile Lys Arg His Glu His Phe Leu Ala Leu Gln Leu
                85                  90                  95
Gly Leu Lys Pro Gly His Lys Val Leu Asp Val Gly Cys Gly Ile Gly
            100                 105                 110
Gly Pro Leu Arg Glu Ile Ala Arg Phe Ser Ser Ala Ser Val Thr Gly
        115                 120                 125
Leu Asn Asn Asn Glu Tyr Gln Ile Thr Arg Gly Lys Glu Leu Asn Arg
    130                 135                 140
Ile Ala Gly Val Asp Lys Thr Cys
145                 150
```

<210> 249
<211> 100
<212> PRT
<213> Eucalyptus grandis

<400> 249
Met Ser Lys Ala Gly Ala Met Asp Leu Ala Thr Gly Leu Gly Gly Lys
1 5 10 15
Met Asp Lys Ser Asp Val Leu Ser Ala Val Asp Lys Tyr Glu Lys Tyr
20 25 30
His Val Cys Tyr Gly Gly Asp Glu Glu Glu Arg Arg Ala Asn Tyr Ser
35 40 45
Asp Met Val Asn Lys Tyr Tyr Asp Leu Ala Thr Ser Phe Tyr Glu Phe
50 55 60
Gly Trp Gly Glu Ser Phe His Phe Ala His Arg Trp Lys Gly Glu Ser
65 70 75 80
Leu Arg Glu Ser Ile Lys Arg His Glu His Phe Leu Ala Leu Gln Leu
85 90 95
Gly Leu Lys Pro
100

<210> 250
<211> 148
<212> PRT
<213> Eucalyptus grandis

<400> 250
Ala Met Pro Trp Tyr Cys Ala Leu Pro Thr Leu Ser Glu Tyr Met Val
1 5 10 15
Glu Asn Gly Trp Thr Lys Cys Phe Ser Arg Ile Ser Asp Val Gly Trp
20 25 30
Leu Ala Tyr Leu Val Tyr Leu Ser Ile Tyr Leu Val Met Ala Glu Phe
35 40 45
Gly Ile Tyr Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr
50 55 60
Lys His Leu His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu
65 70 75 80
Ser Pro Phe Ala Gly Leu Ala Phe His Pro Leu Asp Gly Ile Leu Gln
85 90 95
Ala Val Pro His Val Met Ala Leu Phe Leu Val Pro Thr His Phe Thr
100 105 110
Thr His Ile Ala Leu Leu Phe Leu Glu Ala Ile Trp Thr Ala Asn Ile
115 120 125
His Asp Cys Ile His Gly Lys Leu Trp Pro Val Met Gly Ala Gly Tyr
130 135 140
His Thr Ile His
145

<210> 251
<211> 201
<212> PRT
<213> Eucalyptus grandis

<400> 251
Phe Met Ser Cys Leu Pro Asn Met Ile Val Met Ala Pro Ser Asp Glu
1 5 10 15
Asp Glu Leu Val Asp Met Val Glu Thr Ala Ala Ile Val Asp Asp Arg
20 25 30
Pro Ile Cys Phe Arg Tyr Pro Arg Gly Ala Ile Val Arg Thr Asp Lys
35 40 45

```
Ser Leu Ser Gln Gly Ile Pro Ile Glu Ile Gly Lys Gly Arg Ile Leu
    50                  55                  60
Ala Glu Gly Lys Asp Val Ala Leu Leu Gly Tyr Gly Ser Met Val Gln
65                  70                  75                  80
Asn Cys Val Lys Ala Arg Ser Leu Leu Ser Lys Leu Gly Ile Glu Val
                85                  90                  95
Thr Val Ala Asp Ala Arg Phe Cys Lys Pro Leu Asp Ile Gly Leu Leu
            100                 105                 110
Arg Glu Leu Cys Glu Asn His Ala Phe Leu Val Thr Val Glu Glu Gly
        115                 120                 125
Ser Ile Gly Gly Phe Gly Ser His Val Ala Gln Phe Ile Ala Leu Asp
    130                 135                 140
Gly Arg Leu Asp Gly Arg Ile Lys Trp Arg Pro Ile Val Leu Pro Asp
145                 150                 155                 160
Ala Tyr Val Glu His Ala Ser Pro Asn Glu Gln Leu Ser Leu Ala Gly
                165                 170                 175
Leu Thr Gly His His Ile Ala Ala Thr Val Leu Ser Leu Leu Gly Arg
            180                 185                 190
Thr Arg Glu Ala Leu Leu Leu Met Cys
        195                 200

      <210> 252
      <211> 138
      <212> PRT
      <213> Eucalyptus grandis

      <400> 252
Asp Ile Lys Lys Ile Val Glu Leu Met Ser Asp Leu His Phe Ile Tyr
1               5                   10                  15
Asn Thr His Arg Phe Ala Tyr Leu Tyr Ser Lys Phe Asn Ser Ser Ile
            20                  25                  30
Tyr Met Tyr Lys Phe Ser Leu Asp Thr Asp Leu Asn Ile Val Lys Lys
        35                  40                  45
Met Ser Gly Phe Asp Val Glu Gly Val Cys His Ala Asp Glu Leu Phe
    50                  55                  60
Tyr Phe Phe Ser Thr Asn Met Thr Lys Asp Tyr Tyr Glu Ser Glu Asp
65                  70                  75                  80
Lys Ile Lys Glu Tyr Val Trp Lys Val Thr Lys Leu Trp Thr Asn Phe
                85                  90                  95
Ala Lys Thr Ser Asn Pro Thr Pro Asp Thr Ser Leu Gly Val Ser Trp
            100                 105                 110
Pro Arg Tyr Thr Met Ala Asn Lys Glu Tyr Leu Asp Ile Asn Thr Gln
        115                 120                 125
Leu Thr Thr Gly Arg Tyr Ser Glu Arg Glu
    130                 135

      <210> 253
      <211> 610
      <212> PRT
      <213> Pinus radiata

      <400> 253
Cys Leu Leu Leu Leu Gln Leu Lys Leu Phe Cys Ser Pro Ile Asn Met
1               5                   10                  15
Ala Ile Ala Ser Arg Ala Gly Val Ala Pro Ile Leu Gln Val Asp Cys
            20                  25                  30
His Phe Thr His Phe Asn Ser Met Thr Glu Leu Gly Ser Arg Asn Ser
        35                  40                  45
Met Met Phe Gln Ser Ala Ile Pro Cys Ser Phe Arg Gln Ile Arg Ala
    50                  55                  60
Thr Thr Lys Arg Lys Arg Cys Val Leu Leu Ala Lys Leu Ser Asn Ser
```

```
65                  70                  75                  80
Asp Gly Glu Asn Gly Lys Asn Val Lys Ala Ala Val Glu Ile Ala Ser
                85                  90                  95
Lys Ser Gly Phe Pro Ala Glu Lys Pro Pro Thr Pro Leu Leu Asp Thr
            100                 105                 110
Val Asn Tyr Pro Val His Leu Lys Asn Leu Ser Ile Gln Asp Leu Glu
        115                 120                 125
Gln Leu Ala Thr Glu Ile Arg Ala Glu Leu Val Phe Gly Val Ala Lys
    130                 135                 140
Thr Gly Gly His Leu Gly Gly Ser Leu Gly Val Val Asp Leu Thr Val
145                 150                 155                 160
Ala Leu His His Val Phe Asp Ser Pro Glu Asp Arg Ile Ile Trp Asp
                165                 170                 175
Val Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Ser
            180                 185                 190
Lys Met His Thr Ile Arg Gln Thr Ser Gly Leu Ala Gly Phe Pro Lys
        195                 200                 205
Arg Asp Glu Ser Lys Tyr Asp Ala Phe Gly Ala Gly His Ser Ser Thr
    210                 215                 220
Ser Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Leu Lys
225                 230                 235                 240
Lys Asn Asn His Val Val Ala Val Ile Gly Asp Gly Ala Met Thr Ala
                245                 250                 255
Gly Gln Ala Tyr Glu Ala Met Asn Asn Ser Gly Tyr Leu Glu Ser Asn
            260                 265                 270
Leu Ile Ile Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala
        275                 280                 285
Thr Leu Asp Gly Ala Ala Pro Pro Val Gly Ala Leu Thr Arg Ala Leu
    290                 295                 300
Thr Lys Leu Gln Ser Ser Lys Lys Leu Arg Lys Leu Arg Glu Ala Ala
305                 310                 315                 320
Lys Gly Leu Thr Lys Gln Ile Gly Gly Pro Thr His Glu Val Ala Ser
                325                 330                 335
Lys Val Asp Lys Tyr Ala Arg Gly Leu Ile Ser Pro Ala Ser Ser Ser
            340                 345                 350
Leu Phe Asp Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His
        355                 360                 365
Asn Ile Glu Asp Met Val Thr Ile Leu Glu Lys Ile Lys Ser Met Pro
    370                 375                 380
Ala Thr Gly Pro Val Leu Ile His Leu Val Thr Glu Lys Gly Lys Gly
385                 390                 395                 400
Tyr Pro Pro Ala Glu Glu Ala Ala Asp Lys Leu His Gly Val Val Lys
                405                 410                 415
Phe Asp Pro Val Thr Gly Lys Gln Phe Lys Ser Lys Ser Ser Val Leu
            420                 425                 430
Ser Tyr Thr Gln Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Val
        435                 440                 445
Asp Ser Lys Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly
    450                 455                 460
Leu Asn Tyr Phe Gln Lys Lys Phe Pro Glu Arg Cys Phe Asp Val Gly
465                 470                 475                 480
Ile Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Thr Glu
                485                 490                 495
Gly Leu Lys Pro Phe Cys Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly
            500                 505                 510
Tyr Asp Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg
        515                 520                 525
Phe Ala Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His
    530                 535                 540
Cys Gly Ser Phe Asp Val Ala Tyr Met Ala Cys Leu Pro Asn Met Ile
545                 550                 555                 560
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Val Met Ala Pro Ser Asp Glu Val Glu Leu Met His Ile Val Ala Thr
565 570 575
Ala Ala Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Phe Pro Arg Gly
580 585 590
Asn Gly Val Gly Leu Ser Asn Leu Pro Leu Asn Asn Lys Gly Val Pro
595 600 605
Leu Glu
610

<210> 254
<211> 147
<212> PRT
<213> Eucalyptus grandis

<400> 254
Met Ala Asp Leu Lys Ser Lys Phe Met Glu Ala Tyr Ala Val Leu Lys
1 5 10 15
Lys Glu Leu Leu Ala Asp Pro Ala Phe Glu Phe Ser Asp Glu Ser Arg
20 25 30
Gln Trp Val Asp Arg Met Leu Asp Tyr Asn Val Pro Gly Gly Lys Leu
35 40 45
Asn Arg Gly Leu Ser Val Ile Asp Ser Tyr Lys Leu Leu Lys Glu Gly
50 55 60
Lys Glu Leu Thr Glu Glu Glu Ile Phe Leu Ala Ser Ala Leu Gly Trp
65 70 75 80
Cys Ile Glu Trp Leu Gln Ala Tyr Phe Leu Val Leu Asp Asp Ile Met
85 90 95
Asp Ser Ser His Thr Arg Arg Gly Gln Pro Cys Trp Phe Arg Leu Pro
100 105 110
Lys Val Gly Met Ile Ala Ala Asn Asp Gly Val Leu Leu Arg Asn His
115 120 125
Ile Pro Arg Ile Leu Lys Asn His Phe Arg Gly Lys Pro Tyr Tyr Val
130 135 140
Asp Leu Leu
145

<210> 255
<211> 123
<212> PRT
<213> Eucalyptus grandis

<400> 255
Phe Pro Leu Ser Ser Ser Ser Leu Cys Ser Glu Phe Pro Phe Cys Val
1 5 10 15
Ala Gly Arg Ala Arg Gln Ala Gly Ala Gly Gly Trp Ala Gly Glu Ser
20 25 30
Ser Val Val Ala Ser Met Ala Asp Leu Asn Ser Lys Leu Leu Glu Ala
35 40 45
Asn Ala Val Leu Lys Lys Glu Leu Pro Glu Asp Pro Ala Phe Glu Phe
50 55 60
Ser Asp Asp Ser Arg Gln Trp Val Glu Arg Glu Asn Tyr Gly Lys Pro
65 70 75 80
Asp Ser Ala Asn Val Ala Lys Val Lys Val Leu Tyr His Glu Ile Asn
85 90 95
Leu Gln Gly Tyr Cys Lys Ser Ile Ser Lys Asn Lys Asn Ile Pro Thr
100 105 110
Val Lys Ala Asn Ala Asn Ser Val Glu Ala Thr
115 120

<210> 256
<211> 127

<212> PRT
<213> Pinus radiata

<400> 256
Arg Pro Cys His Leu Glu Trp Ile His Ile His Lys Thr Ala Val Ile
1 5 10 15
Leu Glu Cys Ser Val Val Cys Gly Asp Ile Ile Ser Gly Ala Ser Glu
20 25 30
Asn Glu Ile Glu Arg Ile Lys Ser Tyr Ala Arg Ser Val Gly Leu Leu
35 40 45
Phe Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Lys Glu
50 55 60
Leu Gly Lys Thr Ala Gly Lys Asp Leu Ile Thr Asp Lys Ala Thr Tyr
65 70 75 80
Pro Lys Leu Met Gly Leu Glu Thr Ala Lys Gln Phe Ala Val Glu Leu
85 90 95
Leu Gly Arg Ala Lys Glu Asp Leu Ser Cys Phe Asp Pro Lys Lys Ala
100 105 110
Ala Pro Leu Leu Gly Ile Ala Glu Tyr Ile Ala Phe Arg Gln Asn
115 120 125

<210> 257
<211> 196
<212> PRT
<213> Eucalyptus grandis

<400> 257
Ala Cys Ala Val Glu Met Ile His Thr Met Ser Leu Ile His Asp Asp
1 5 10 15
Leu Pro Cys Met Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr Asn
20 25 30
His Lys Val Tyr Gly Glu Asp Val Ala Val Leu Ala Gly Asp Ala Leu
35 40 45
Leu Ala Tyr Ala Phe Glu His Ile Ala Val Glu Thr Lys Gly Val Ser
50 55 60
Pro Thr Arg Ile Val Arg Ala Ile Phe Glu Leu Ala Arg Ser Ile Gly
65 70 75 80
Ala Glu Gly Leu Val Ala Gly Gln Val Val Asp Ile Ser Ser Glu Gly
85 90 95
Ile Ala Asn Val Gly Leu Glu His Leu Glu Phe Ile His Leu His Lys
100 105 110
Thr Ala Ala Leu Leu Glu Ala Ser Val Val Leu Gly Ala Ile Met Gly
115 120 125
Gly Gly Ser Asn Glu Glu Val Glu Lys Leu Arg Gly Phe Ala Arg Cys
130 135 140
Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp Leu Thr Gln
145 150 155 160
Ser Ser Gln Glu Leu Gly Lys Thr Ala Gly Lys Asp Leu Val Ala Asp
165 170 175
Lys Val Thr Tyr Pro Lys Leu Met Gly Ile Glu Lys Ser Arg Glu Leu
180 185 190
Ala Asn Lys Leu
195

<210> 258
<211> 159
<212> PRT
<213> Eucalyptus grandis

<400> 258
Met Gly Ser Leu Gly Ala Ile Leu Lys His Pro Asp Asp Phe Tyr Pro

```
1               5                   10                  15
Leu Leu Lys Leu Lys Ile Ala Ala Arg Asn Ala Glu Lys Arg Ile Pro
            20                  25                  30
Pro Gln Pro His Trp Gly Phe Cys Tyr Ser Met Leu His Lys Val Ser
        35                  40                  45
Arg Ser Phe Gly Leu Val Ile Gln Gln Leu Gly Pro Glu Leu Arg Asp
    50                  55                  60
Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
65                  70                  75                  80
Asp Asp Thr Ser Ile Pro Thr Asp Val Lys Val Pro Ile Leu Lys Ala
                85                  90                  95
Phe His Gln His Val Tyr Asp Lys Glu Trp His Phe Ser Cys Gly Thr
            100                 105                 110
Lys Glu Tyr Lys Val Leu Met Asp Gln Phe His His Val Ser Thr Ala
        115                 120                 125
Phe Leu Glu Leu Gly Lys Ser Tyr Gln Glu Ala Ile Asp Asp Ile Thr
    130                 135                 140
Lys Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Gln Glu Val
145                 150                 155

<210> 259
<211> 106
<212> PRT
<213> Pinus radiata

<400> 259
Met Ala Ile Tyr Thr Pro Gln Pro Ala His Arg Leu Ile Ser Trp Ser
1               5                   10                  15
Thr Met Glu Asn His Thr Val Ala Ile Ala Val Ala Ile Gly Phe Val
            20                  25                  30
Ser Val Leu Leu Ser Tyr Tyr Ile Val Leu Asn Arg Trp Lys Arg Arg
        35                  40                  45
Ser Asn Gly Leu Arg Gly Ile Gln Ser Lys Ser Phe Glu Lys Ser Thr
    50                  55                  60
Asp Asp Asn Gly Ile Ala Ile Glu Ala Ala Gly Gly Thr Asp Val Ile
65                  70                  75                  80
Ile Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly
                85                  90                  95
Lys Asp Gly Arg Arg Ile His Val Ile Glu
            100                 105

<210> 260
<211> 93
<212> PRT
<213> Pinus radiata

<400> 260
Met Ala Ile Tyr Thr Pro Gln Pro Ala His Arg Leu Ile Ser Trp Ser
1               5                   10                  15
Thr Met Glu Asn His Thr Val Val Ile Ala Ala Ala Ile Ser Phe Val
            20                  25                  30
Ser Val Leu Leu Ser Tyr Tyr Ile Val Leu Ser Arg Trp Lys Arg Arg
        35                  40                  45
Ser Asn Gly Leu Arg Gly Ile Gln Ser Lys Ser Phe Glu Lys Ser Thr
    50                  55                  60
Asp Asp Asn Gly Ile Ala Ile Glu Ala Ala Gly Gly Thr Asp Val Ile
65                  70                  75                  80
Ile Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr
                85                  90

<210> 261
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<211> 217
<212> PRT
<213> Eucalyptus grandis

<400> 261
Pro Gln Leu Tyr Lys Ala Phe Ile Ala Ala Ile Asp Lys Gly Asn Ile
1 5 10 15
Lys Ser Met Pro Asn Arg Ser Met Pro Ala Asn Pro Gln Pro Thr Pro
20 25 30
Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr
35 40 45
Gly Gly Gly Met Thr Val Ala Leu Ser Asp Ile Val Leu Leu Arg Asn
50 55 60
Leu Leu Arg Pro Leu Gln Asp Leu Asn Asp Ala Ser Ala Leu Cys Lys
65 70 75 80
Tyr Leu Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile
85 90 95
Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala Ser Pro Asp
100 105 110
Pro Ala Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser Leu
115 120 125
Gly Gly Leu Cys Ser Thr Gly Pro Val Ser Leu Leu Ser Gly Leu Asn
130 135 140
Pro Arg Pro Met His Leu Val Cys His Phe Phe Ala Val Ala Val Tyr
145 150 155 160
Gly Val Gly Arg Leu Cys Leu Pro Phe Pro Ser Pro Lys Arg Met Trp
165 170 175
Leu Gly Ala Arg Leu Val Lys Gly Ala Ser Gly Ile Ile Phe Pro Ile
180 185 190
Ile Arg Asp Glu Gly Val Arg Gln Met Phe Phe Pro Ala Thr Val Pro
195 200 205
Ala Tyr His Arg Ala Pro Pro Val His
210 215

<210> 262
<211> 94
<212> PRT
<213> Eucalyptus grandis

<400> 262
Met Glu Asp Asp Arg Asp Arg Gly Leu Leu Tyr Asp Ser Asp Pro Ser
1 5 10 15
Ser Ser Ser Leu Ser Pro Pro Arg Pro Phe Ala Leu Thr Phe Phe Asp
20 25 30
Arg Glu Arg His Val Thr Phe Leu Glu Met Met Tyr His Met Leu Pro
35 40 45
Arg Pro Tyr Gln Ser Gln Glu Ile Asn His Leu Thr Leu Ala Tyr Phe
50 55 60
Val Ile Ser Gly Leu Asp Ile Leu Asp Ala Leu Asp Arg Val His Lys
65 70 75 80
Asp Ala Val Ala Asp Trp Val Leu Ser Phe Gln Ala His Phe
85 90

<210> 263
<211> 81
<212> PRT
<213> Eucalyptus grandis

<400> 263
Glu Ile Leu Thr Lys Val Ile Ser Leu Ala Ser Ile Met Asp Asp Ile
1 5 10 15

Tyr Asp Val Tyr Gly Thr Leu Glu Glu Leu Ala Leu Leu Asn Glu Ala
20 25 30
Ile Gln Lys Trp Asp Phe Asp Ala Met Asp Gly Leu Pro Glu Tyr Met
35 40 45
Gln Ala Tyr Phe Lys Glu Phe Leu Gln Leu Tyr Glu Tyr Ile Gly Asn
50 55 60
Gln Leu Ala Ala Lys Gly Arg Ser Tyr Arg Leu Ile Tyr Ala Lys Glu
65 70 75 80
Val

<210> 264
<211> 125
<212> PRT
<213> Pinus radiata

<400> 264
Leu Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Asp
1 5 10 15
Glu Ala Glu Thr Phe Ser Ala Lys Tyr Leu Lys Glu Ala Leu Gln Lys
20 25 30
Ile Pro Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr
35 40 45
Gly Trp His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp
50 55 60
Val Phe Gly Gln Asp Thr Glu Asn Ser Lys Ser Tyr Met Lys Thr Glu
65 70 75 80
Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ala Leu
85 90 95
Gln Lys Arg Glu Leu Glu Tyr Leu Val Arg Trp Trp Lys Gly Ser Gly
100 105 110
Ser Pro Gln Met Thr Phe Cys Arg His Arg His Val Glu
115 120 125

<210> 265
<211> 219
<212> PRT
<213> Pinus radiata

<400> 265
Met Pro Gln Asp Met Lys Ile Cys Phe Lys Gly Phe Tyr Asn Thr Phe
1 5 10 15
Asn Glu Ile Ala Glu Glu Gly Arg Lys Arg Gln Gly Arg Asp Val Leu
20 25 30
Ser Tyr Ile Gln Lys Val Trp Glu Val Gln Leu Glu Ala Tyr Thr Lys
35 40 45
Glu Ala Glu Trp Ser Ala Val Arg Tyr Val Pro Ser Tyr Asp Glu Tyr
50 55 60
Ile Gly Asn Ala Ser Val Ser Ile Ala Leu Gly Thr Val Val Leu Ile
65 70 75 80
Ser Ala Leu Phe Thr Gly Glu Ile Leu Thr Asp Asp Ile Leu Ser Lys
85 90 95
Ile Gly Arg Asp Ser Arg Phe Leu Tyr Leu Met Gly Leu Thr Gly Arg
100 105 110
Leu Val Asn Asp Thr Lys Thr Tyr Gln Ala Glu Arg Gly Gln Gly Glu
115 120 125
Val Ala Ser Ala Val Gln Cys Tyr Met Lys Asp His Pro Glu Ile Ser
130 135 140
Glu Glu Glu Ala Leu Lys His Val Tyr Thr Ile Met Asp Asn Ala Leu
145 150 155 160
Asp Glu Leu Asn Arg Glu Phe Val Asn Asn Arg Asp Val Pro Asp Thr

```
                165                 170                 175
Cys Arg Arg Leu Val Phe Glu Thr Ala Arg Ile Met Gln Leu Phe Tyr
            180                 185                 190
Met Asp Gly Asp Gly Leu Thr Leu Ser His Asn Met Glu Ile Lys Glu
        195                 200                 205
His Val Lys Asn Cys Leu Phe Gln Pro Val Ala
    210                 215

    <210> 266
    <211> 423
    <212> PRT
    <213> Eucalyptus grandis

    <400> 266
Leu Asp Cys Glu Pro Val Val Gln Lys Pro Lys Leu Val Asp Pro Val
1               5                   10                  15
Val Gln Asp Ala Pro Lys Glu Lys Val Ile Glu Ala Val Pro Ser Ala
            20                  25                  30
Met Pro Glu Glu Asp Glu Glu Ile Ile Lys Ser Val Val Glu Gly Lys
        35                  40                  45
Met Pro Ser Tyr Ser Leu Glu Ser Lys Leu Gly Asp Cys Lys Arg Ala
    50                  55                  60
Ala Ala Ile Arg Arg Glu Ala Leu Gln Arg Ile Thr Gly Lys Ser Leu
65                  70                  75                  80
Ser Gly Leu Pro Leu Glu Gly Phe Asp Tyr Glu Ser Ile Leu Gly Gln
                85                  90                  95
Cys Cys Glu Met Pro Val Gly Tyr Val Gln Ile Pro Val Gly Ile Ala
            100                 105                 110
Gly Pro Leu Leu Leu Asp Gly Arg Glu Tyr Ser Val Pro Met Ala Thr
        115                 120                 125
Thr Glu Gly Cys Leu Val Ala Ser Thr Asn Arg Gly Cys Lys Ala Ile
    130                 135                 140
Phe Val Ser Gly Gly Ala Thr Ser Val Leu Leu Arg Asp Gly Met Thr
145                 150                 155                 160
Arg Ala Pro Ile Val Arg Phe Gly Thr Ala Lys Arg Ala Ala Asp Leu
                165                 170                 175
Lys Phe Phe Val Glu Asn Pro Ala Asn Phe Glu Ser Leu Ala Val Ile
            180                 185                 190
Phe Asn Arg Ser Ser Arg Phe Ala Arg Leu Gln Ser Ile Lys Cys Ala
        195                 200                 205
Ile Ala Gly Lys Asn Leu Tyr Met Arg Phe Ser Cys Ser Thr Gly Asp
    210                 215                 220
Ala Met Gly Met Asn Met Val Ser Lys Gly Val Gln Asn Val Leu Asp
225                 230                 235                 240
Phe Leu Gln Ser Asp Phe Pro Asp Met Asp Val Leu Gly Ile Ser Gly
                245                 250                 255
Asn Phe Cys Ala Asp Lys Lys Pro Ala Ala Val Asn Trp Ile Glu Gly
            260                 265                 270
Arg Gly Lys Ser Val Val Cys Glu Ala Thr Ile Lys Gly Asp Val Val
        275                 280                 285
Arg Lys Val Leu Lys Thr Ser Val Glu Ala Leu Val Glu Leu Asn Met
    290                 295                 300
Leu Lys Asn Leu Thr Gly Ser Ala Met Ala Gly Ala Leu Gly Gly Phe
305                 310                 315                 320
Asn Ala His Ala Ser Asn Ile Val Ala Ala Ile Phe Ile Ala Thr Gly
                325                 330                 335
Gln Asp Pro Ala Gln Asn Val Glu Ser Ser His Cys Ile Thr Met Met
            340                 345                 350
Glu Ala Ile Asn Asp Gly Lys Asp Leu His Val Ser Val Thr Met Pro
        355                 360                 365
Ser Ile Glu Val Gly Thr Val Gly Gly Gly Thr Gln Leu Ala Ser Gln
```

370 375 380
Ser Ala Cys Leu Asn Leu Leu Gly Val Lys Gly Ala Asn Lys Glu Leu
385 390 395 400
Ala Gly Ala Asn Ser Arg Leu Leu Ala Thr Val Val Ser Gly Ala Val
405 410 415
Leu Ala Ala Glu Leu Ser Ser
420

<210> 267
<211> 112
<212> PRT
<213> Pinus radiata

<400> 267
Met Ser Leu Ile Ser Ala Val Pro Leu Ala Ser Ser Cys Val Ser Lys
1 5 10 15
Ser Leu Ile Ser Ser Val Arg Glu His Lys Ala Leu Arg Arg Ala Ile
20 25 30
Ala Thr Leu Gln Met Ser Arg Pro Gly Lys Ser Val Ala Ala Ser Thr
35 40 45
Arg Met Ser Ser Ala Thr Ala Gly Ser Asp Asp Gly Val Lys Arg Arg
50 55 60
Ile Gly Asp Tyr His Ser Asn Leu Trp Glu Asp Asn Phe Ile Gln Ser
65 70 75 80
Leu Ser Ser Pro Tyr Gly Ala Ser Ser Tyr Gly Glu His Ala Asp Arg
85 90 95
Leu Ile Gly Glu Val Lys Gly Ile Phe Asn Ser Phe Ser Ile Ala Asp
100 105 110

<210> 268
<211> 165
<212> PRT
<213> Pinus radiata

<400> 268
Met Ser Leu Ile Ser Ala Val Pro Leu Ala Ser Ser Ser Val Ser Lys
1 5 10 15
Ser Leu Ile Ser Ser Val Arg Glu His Lys Ala Leu Arg Arg Ala Ile
20 25 30
Ala Thr Leu Gln Met Ser Arg Pro Gly Lys Ser Val Ala Ala Ser Thr
35 40 45
Lys Met Ser Ser Ala Thr Ala Gly Ser Asp Asp Gly Val Lys Arg Arg
50 55 60
Ile Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asn Val Ile Gln Ser
65 70 75 80
Leu Ser Ser Pro Tyr Gly Ala Ser Ser Tyr Gly Glu His Ala Asp Arg
85 90 95
Leu Ile Gly Glu Val Lys Glu Ile Phe Asn Ser Phe Ser Ile Ala Asp
100 105 110
Gly Glu Leu Thr Ser Pro Val Asn Asp Leu Leu Gln Gln Leu Trp Met
115 120 125
Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Gln Thr Glu
130 135 140
Ile Lys Val Ala Leu Asp Tyr Gly Tyr Arg Tyr Trp Ser Glu Lys Gly
145 150 155 160
Ile Glu Cys Gly Glu
165

<210> 269
<211> 144
<212> PRT

<213> Pinus radiata

<400> 269

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Ser Thr Leu Gln Leu Ser Arg Arg Gly Lys Pro Val Thr Ala Cys Lys
1               5                   10                  15
Lys Val Ser Leu Ser Thr Ala Val Ser Asp Asp Gly Ala Lys Arg Arg
            20                  25                  30
Val Gly Asp His His Ser Asn Leu Trp Asp Asp Asn Phe Ile Lys Ser
        35                  40                  45
Leu Ser Ser Pro Tyr Gly Ala Ser Ser Tyr Arg Glu His Ala Asp Arg
    50                  55                  60
Val Ile Gly Glu Val Lys Glu Ile Phe Asn Ser Leu Ser Met Thr Asp
65                  70                  75                  80
Gly Glu Leu Ile Ser Pro Asp Asn Asp Leu Leu Gln Arg Leu Ser Met
                85                  90                  95
Val Asp Asn Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Thr Glu
            100                 105                 110
Ile Lys Leu Thr Leu Asp Tyr Val Tyr Ser Tyr Trp Ser Glu Lys Gly
        115                 120                 125
Ile Gly Tyr Gly Arg Glu Ser Ala Ile Thr Asp Leu Asn Thr Thr Ser
    130                 135                 140
```

<210> 270
<211> 106
<212> PRT
<213> Pinus radiata

<400> 270

```
Gly Thr Lys Ala Lys Gly Asn Lys Gln Leu Gln Asn Asn Val Ile Lys
1               5                   10                  15
Val Ile Cys Asn Thr Asp Lys Ser Arg Gly Phe Asn Val Leu Arg Asp
            20                  25                  30
Val Ser Met Pro Gln Ile Met Ile Lys Ser Cys Lys Val Ser Pro Asp
        35                  40                  45
Ala Arg Pro Tyr Gln Asn Leu Gly Gly Pro Ala Ser Ser Glu Arg Pro
    50                  55                  60
Phe Leu Ala Phe Phe Ala Gly Gln Met His Gly Thr Leu Arg Pro Glu
65                  70                  75                  80
Ile Leu Lys His Trp Gly Asn Glu Thr Asp Pro Asn Met Lys Ile Phe
                85                  90                  95
Ala Val Gly Gln Ser His Pro Gly Ser Leu
            100                 105
```

<210> 271
<211> 169
<212> PRT
<213> Eucalyptus grandis

<400> 271

```
Lys Ala Arg Ala Val Trp Glu Asn Phe Lys Asp Asn Pro Leu Phe Asp
1               5                   10                  15
Ile Ser Thr Asp His Pro Thr Thr Tyr Tyr Glu Asp Met Gln Arg Ala
            20                  25                  30
Val Phe Cys Leu Cys Pro Leu Gly Trp Ala Pro Trp Ser Pro Arg Leu
        35                  40                  45
Val Glu Ala Val Val Phe Gly Cys Ile Pro Val Ile Ile Ala Asp Asp
    50                  55                  60
Ile Val Leu Pro Phe Ala Asp Ala Ile Pro Trp Glu Glu Ile Gly Val
65                  70                  75                  80
Phe Val Ala Glu Glu Asp Val Pro Ser Leu Asp Thr Ile Leu Thr Ser
                85                  90                  95
```

```
Ile Ser Pro Glu Val Ile Leu Arg Lys Gln Arg Leu Leu Ala Asn Pro
            100                 105                 110
Ser Met Lys Arg Ala Met Leu Phe Pro Gln Pro Ala Gln Ser Gly Asp
        115                 120                 125
Ala Phe His Gln Ile Leu Asn Gly Leu Ala Arg Lys Leu Pro His His
    130                 135                 140
Arg Ser Val Tyr Leu Lys Pro Gly Glu Lys Val Leu Asn Trp Thr Ala
145                 150                 155                 160
Gly Pro Val Gly Asp Leu Lys Pro Trp
                165

      <210> 272
      <211> 146
      <212> PRT
      <213> Eucalyptus grandis

      <400> 272
Met Ser Gln Val Ser Ala Thr Pro Cys Ala Pro Pro Asn Lys Glu Thr
 1               5                  10                  15
Gly His Val Ile Glu Arg Arg Ser Ala Gly Tyr His Pro Ser Val Trp
            20                  25                  30
Gly Asp Tyr Phe Leu Lys Tyr Asp Ser Pro Ser Asn Ser Val Lys Phe
        35                  40                  45
Lys Phe Leu Gly Arg Val Glu Gly Gln Ile Glu Glu Leu Lys Gly Glu
    50                  55                  60
Val Lys Lys Met Leu Ile Asp Val Val Asp Lys Pro Leu Pro Lys Leu
65                  70                  75                  80
His Leu Ile Asp Gln Ile Gln Arg Leu Gly Ile Glu Tyr His Phe Glu
                85                  90                  95
Arg Glu Val Asp Glu Gln Leu Glu Gln Ile His Lys Ser Tyr Ser Arg
            100                 105                 110
Leu Asp His Glu Asp Phe Lys Val Asp Asp Leu His Met Val Ala Leu
        115                 120                 125
Ile Phe Arg Leu Leu Arg Gln His Gly Tyr Asn Ile Ser Ser Glu Ile
    130                 135                 140
Phe Asp
145

      <210> 273
      <211> 132
      <212> PRT
      <213> Eucalyptus grandis

      <400> 273
Lys Lys Met Leu Ile Asp Ala Val Asp Lys Pro Leu Pro Lys Leu His
 1               5                  10                  15
Leu Ile Asp Gln Ile Gln Arg Leu Gly Ile Glu Tyr His Phe Glu Arg
            20                  25                  30
Glu Val Asp Glu Gln Leu Glu Gln Ile His Lys Ser Tyr Ser Arg Leu
        35                  40                  45
Asp His Glu Asp Phe Lys Val Asp Asp Leu His Thr Val Ala Leu Ile
    50                  55                  60
Phe Arg Leu Leu Arg Gln His Gly Tyr Asn Ile Ser Ser Glu Val Phe
65                  70                  75                  80
Asp Lys Phe Lys Ile Ala Thr Gly Thr Ser Glu Ser Arg Leu Ile Ser
                85                  90                  95
Asp Val Arg Gly Leu Leu Ser Leu Tyr Glu Ala Cys His Leu Arg Cys
            100                 105                 110
His Gly Asp Ser Ile Leu Asp Glu Ala Leu Pro Phe Ala Thr Thr His
        115                 120                 125
Leu Glu Ser Ile
```

130

<210> 274
<211> 116
<212> PRT
<213> Eucalyptus grandis

<400> 274
Met Ser Gln Val Ser Ala Thr Pro Cys Ala Pro Ser Asn Lys Gly Thr
1   5   10   15
Gly His Val Ile Glu Arg Arg Ser Ala Gly Tyr His Pro Ser Val Trp
            20   25   30
Gly Asp Tyr Phe Leu Lys Tyr Asp Ser Pro Ser Asn Ser Val Lys Phe
        35   40   45
Lys Phe Leu Gly Arg Val Glu Gly Gln Ile Glu Glu Leu Lys Gly Glu
    50   55   60
Val Lys Lys Met Leu Thr Asp Ile Met Asp Lys Pro Leu Gln Lys Leu
65   70   75   80
His Leu Ile Asp Gln Ile Gln Arg Leu Gly Ile Glu Tyr His Phe Glu
                85   90   95
Arg Glu Ile Asp Glu Gln Leu Glu Gln Ile His Lys Ser Tyr Ser Arg
            100   105   110
Leu Asp His Glu
        115

<210> 275
<211> 214
<212> PRT
<213> Pinus radiata

<400> 275
Met Ala Thr Phe Ser Asp Glu Thr Pro Val Ser Ser Leu Ala Cys Gly
1   5   10   15
Leu Ser Ser Asn Ser Gly Leu Ile Arg Arg Thr Ala Asn Pro His Pro
            20   25   30
Asn Val Trp Gly Tyr Glu Phe Val Asn Ser Leu Lys Ser Pro Tyr Ala
        35   40   45
Asn Ser Ser Tyr Arg Glu Arg Ala Glu Thr Leu Val Ser Glu Ile Lys
    50   55   60
Ala Met Leu Asn Thr Ala Ile Ala Gly Asp Gly Asp Leu Met Ile Thr
65   70   75   80
Pro Ser Ala Tyr Asp Thr Ala Trp Ile Ala Arg Val Pro Ala Ile Asp
                85   90   95
Gly Ser Pro Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys
            100   105   110
Asn Gln Leu Lys Asp Gly Ser Trp Gly Thr Gln Ser His Phe Leu Leu
        115   120   125
Ser Asp Arg Leu Leu Ala Thr Leu Ser Cys Val Leu Ala Leu Leu Lys
    130   135   140
Trp Lys Val Gly Asp Ala Gln Val Gln Gln Gly Ile Lys Phe Ile Arg
145   150   155   160
Ser Asn Leu Leu Lys Asp Glu Ser Asp Glu Asp Ser Leu Val Thr Asp
                165   170   175
Phe Glu Val Asn Phe Pro Phe Leu Leu Arg Glu Ala Gln Ser Phe Gln
            180   185   190
Leu Glu Leu Pro Tyr Asp Leu Pro Tyr Ile His Lys Leu Gln Met Lys
        195   200   205
Arg Gln Glu Arg Leu Ala
    210

<210> 276

<211> 462
<212> PRT
<213> Pinus radiata

<400> 276
Arg Asp Ser Ala Phe Thr Asp Leu Asn Thr Thr Ala Leu Gly Phe Arg
1 5 10 15
Ile Phe Arg Leu His Gly Tyr Thr Val Ser Ser Asp Ala Phe Glu His
20 25 30
Phe Lys Asp Gln Met Gly Gln Phe Ser Ala Ser Ala Asn Asp Thr Glu
35 40 45
Leu Gln Ile Arg Ser Val Phe Asn Leu Phe Arg Ala Ser Leu Ile Ala
50 55 60
Phe Pro Glu Glu Lys Val Leu Glu Glu Ala Glu Asn Phe Ala Ala Ala
65 70 75 80
Tyr Leu Lys Ala Ala Leu Gln Thr Leu Pro Val Ser Gly Leu Ser Arg
85 90 95
Glu Ile Gln Tyr Val Phe Asp Tyr Arg Trp His Ser Asn Leu Pro Arg
100 105 110
Leu Glu Ala Arg Ser Tyr Val Asp Ile Leu Ala Asp Asn Thr Ile Ser
115 120 125
Gly Thr Pro Asp Ala Asn Thr Lys Lys Leu Leu Glu Leu Ala Lys Leu
130 135 140
Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Cys Leu
145 150 155 160
Trp Arg Trp Trp Lys Glu Trp Gly Cys Pro Glu Leu Thr Phe Val Arg
165 170 175
His Arg Tyr Val Glu Phe Tyr Thr Leu Val Ser Gly Thr Asp Met Val
180 185 190
Pro Glu His Ala Ala Phe Arg Leu Ser Phe Val Lys Thr Cys His Leu
195 200 205
Ile Thr Ile Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Ile Asp Glu
210 215 220
Leu Arg Leu Phe Thr Ala Ala Val Lys Arg Trp Asp Pro Ser Ala Thr
225 230 235 240
Glu Cys Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Val Leu Tyr Glu
245 250 255
Thr Val Asn Glu Met Ala Lys Glu Ala Gln Lys Ser Gln Gly Arg Asp
260 265 270
Thr Leu Gly Tyr Val Arg Gln Ala Leu Glu Asp Tyr Ile Gly Ser Tyr
275 280 285
Leu Lys Glu Ala Glu Trp Ile Ala Thr Gly Tyr Val Pro Thr Phe Gln
290 295 300
Glu Tyr Phe Glu Asn Gly Lys Leu Ser Ser Gly His Arg Ile Ala Thr
305 310 315 320
Leu Gln Pro Ile Leu Thr Leu Ser Ile Pro Phe Pro His His Ile Leu
325 330 335
Gln Glu Ile Asp Phe Pro Ser Lys Phe Asn Asp Tyr Ala Cys Ser Ile
340 345 350
Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Ser Ala Arg
355 360 365
Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys Glu Asn Pro Gly
370 375 380
Ser Thr Gln Glu Asp Ala Leu His His Ile Asn Gly Met Ile Glu Asp
385 390 395 400
Met Ile Lys Lys Leu Asn Trp Glu Phe Leu Lys Pro Asp Asn Asn Ala
405 410 415
Pro Ile Ser Ser Lys Lys Asn Ala Phe Asn Ile Ser Arg Gly Leu His
420 425 430
His Phe Tyr Asn Tyr Arg Asp Gly Tyr Ser Val Ala Ser Asn Glu Thr
435 440 445

Lys Asp Leu Val Ile Lys Thr Val Leu Glu Pro Val Leu Met
450 455 460

<210> 277
<211> 98
<212> PRT
<213> Pinus radiata

<400> 277
Leu Gly Glu Asp Ser Leu Thr Gly Thr Pro Asp Val Asn Thr Lys Lys
1 5 10 15
Leu Leu Glu Leu Ser Lys Leu Glu Phe Asn Ile Phe His Ser Val Gln
20 25 30
Gln Lys Glu Leu Gln Cys Leu Ser Arg Trp Trp Lys Glu Ser Gly Ser
35 40 45
Pro Glu Leu Thr Phe Ala Arg His Arg Tyr Val Glu Phe Tyr Thr Leu
50 55 60
Val Cys Gly Ile Asp Met Glu Pro Lys Asp Ala Ala Phe Arg Leu Ser
65 70 75 80
Phe Val Lys Met Cys His Leu Ile Thr Ile Leu Asp Asp Ile Tyr Asp
85 90 95
Thr Phe

<210> 278
<211> 63
<212> PRT
<213> Pinus radiata

<400> 278
Thr Glu Cys Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Val Leu Tyr
1 5 10 15
Glu Thr Val Asn Glu Met Ala Lys Glu Ala Gln Lys Ser Gln Gly Arg
20 25 30
Asp Thr Leu Gly Tyr Val Arg Gln Ala Val Ile Thr Ile Asp Met Leu
35 40 45
Cys Ile Tyr Leu Asn Lys Gln Ile Leu Val Gly His Leu Phe Tyr
50 55 60

<210> 279
<211> 124
<212> PRT
<213> Pinus radiata

<400> 279
Ala Asp Leu Leu Asp Glu Cys Gly Pro Leu Leu Lys Lys Ala His Ala
1 5 10 15
Phe Leu Glu Lys Ser Gln Val Gln Glu Asn Ser Pro Gly Glu Phe Ser
20 25 30
Thr Trp Tyr Arg His Ile Ser Lys Gly Ala Trp Thr Leu Ser Thr Arg
35 40 45
Asp His Gly Trp Val Val Ala Asp Cys Ser Ala Glu Gly Leu Lys Ala
50 55 60
Ala Leu Glu Leu Ser Gln Leu Pro Glu Asn Ile Val Gly Lys Pro Leu
65 70 75 80
Pro Gln Gln Arg Leu Phe Ala Cys Val Asn Tyr Leu Leu Ser Met Gln
85 90 95
Asn Thr Asp Gly Gly Tyr Ala Thr Tyr Asp Leu Thr Arg Ser Tyr Asn
100 105 110
Trp Leu Gly Thr Phe Asn Pro Ala Ala Ile Leu Gly
115 120

<210> 280
<211> 380
<212> PRT
<213> Eucalyptus grandis

<400> 280
Met Asp Thr Asp Asn Lys Leu Phe Asn Val Gly Val Leu Leu Val Ala
1 5 10 15
Thr Leu Val Val Ala Lys Leu Ile Ser Ala Leu Leu Ile Pro Arg Ser
20 25 30
Gly Lys Arg Leu Pro Pro Val Val Arg Thr Trp Pro Val Val Gly Gly
35 40 45
Leu Leu Arg Phe Leu Lys Gly Pro Met Val Met Leu Arg Glu Glu Tyr
50 55 60
Pro Lys Leu Gly Ser Val Phe Thr Leu Asn Leu Leu Asn Lys Lys Ile
65 70 75 80
Thr Phe Phe Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser
85 90 95
Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr
100 105 110
Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Thr Ile Arg Gln Glu
115 120 125
Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Ile Asn Lys Leu Lys Gly
130 135 140
Tyr Val Asn Gln Met Val Met Glu Ala Glu Asp Tyr Phe Ser Lys Trp
145 150 155 160
Gly Asp Ser Gly Glu Val Asp Leu Lys Tyr Glu Leu Glu His Leu Thr
165 170 175
Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu Val Arg Glu Lys
180 185 190
Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu Asp Asn Gly Met
195 200 205
Leu Pro Ile Ser Val Ile Phe Pro Tyr Leu Pro Ile Pro Ala His His
210 215 220
Arg Arg Asp Lys Ala Arg Lys Lys Leu Ser Glu Ile Phe Ala Asn Ile
225 230 235 240
Ile Ser Ser Arg Lys Cys Ala Gly Lys Ser Glu Glu Asp Met Leu Gln
245 250 255
Cys Phe Ile Asp Ser Lys Tyr Lys Asn Gly Arg Pro Thr Thr Glu Ala
260 265 270
Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala Gly Gln His Thr
275 280 285
Ser Ser Ile Thr Ser Val Trp Thr Gly Ala Tyr Leu Leu Thr Asn Lys
290 295 300
Lys Tyr Leu Ser Ala Val Ser Asn Glu Gln Lys His Leu Met Glu Lys
305 310 315 320
His Gly Asn Asn Val Asp His Asp Val Leu Ser Glu Met Asp Val Leu
325 330 335
Tyr Arg Ser Ile Lys Glu Ala Leu Arg Leu His Pro Pro Leu Ile Met
340 345 350
Leu Leu Arg Ser Ser His Ser Asp Phe Ser Val Lys Thr Arg Asp Gly
355 360 365
Lys Glu Tyr Glu Val Gly Glu Val Ser Val Leu Pro
370 375 380

<210> 281
<211> 177
<212> PRT
<213> Eucalyptus grandis

<400> 281

Met Trp Lys Leu Lys Ile Gly Glu Gly Ala Asn Asp Pro Tyr Leu Phe
1 5 10 15
Ser Leu Asn Asn Phe Val Gly Arg Gln Ile Trp Glu Phe Asp Pro Glu
20 25 30
Ala Gly Thr Pro Glu Glu Arg Ala Glu Val Glu Ala Ala Arg Gln Asn
35 40 45
Phe Tyr Asn Asn Arg Phe Lys Val Arg Pro Ser Ser Asp Leu Phe Trp
50 55 60
Arg Phe Gln Phe Leu Arg Glu Lys Asn Phe Lys Gln Thr Ile Pro Pro
65 70 75 80
Val Lys Ile Glu Asp Gly Glu Asp Ile Thr Tyr Glu Lys Ala Thr Ala
85 90 95
Ala Val Lys Arg Cys Val Ser Phe Trp Ser Thr Leu Gln Ser Ser His
100 105 110
Gly His Trp Pro Ala Glu Asn Ala Gly Pro Ile Ala Phe Tyr Phe Pro
115 120 125
Pro Leu Val Met Ser Leu Tyr Val Thr Gly His Leu Asn Asn Val Phe
130 135 140
His Ala Glu His Arg Arg Glu Ile Leu Arg Tyr Ile Tyr Tyr His Gln
145 150 155 160
Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly His Ser Thr Met
165 170 175
Ile

<210> 282
<211> 91
<212> PRT
<213> Pinus radiata

<400> 282

His Ala Arg Gly Leu Gly Pro Pro Pro Ile Pro Val Asp Gln Phe Ser
1 5 10 15
Leu Ala Lys Leu Val Asp Ala Ile Gln Ile Met Leu Asn Pro Gln Val
20 25 30
Lys Asn Asn Ala Asp Ala Ile Ala Lys Ala Met Glu Asn Glu Asp Gly
35 40 45
Val Ser Gly Ala Val Lys Ala Phe His Lys His Leu Pro Lys Lys Met
50 55 60
Pro Gln Pro Leu Pro Pro Pro Thr Asp His Ser Leu Ile Asp Ser Phe
65 70 75 80
Phe Thr Gly Val Gly Lys Val Phe Gly Cys Gly
85 90

<210> 283
<211> 172
<212> PRT
<213> Pinus radiata

<400> 283

Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala Ile Ile Thr
1 5 10 15
Glu Ala Val Val Ser Lys Val Leu Lys Thr Thr Val Pro Ala Leu Leu
20 25 30
Glu Leu Asn Met Leu Lys Asn Leu Thr Gly Ser Ala Leu Ala Gly Ala
35 40 45
Met Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser Ala Val Phe
50 55 60
Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Ile Glu Ser Ser His Cys
65 70 75 80

Ile Thr Met Met Glu Ala Ser Asn Asp Gly Lys Asp Leu His Val Ser
85 90 95
Val Thr Met Pro Cys Ile Glu Val Gly Thr Val Gly Gly Gly Thr Gln
100 105 110
Leu Ala Ser Gln Ala Ala Cys Leu Asn Met Leu Gly Val Lys Gly Ala
115 120 125
Asn Lys Glu Ser Pro Gly Ala Asn Ala Gln Thr Leu Ala Arg Ile Val
130 135 140
Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser Ala Leu Ala
145 150 155 160
Ala Gly Gln Leu Val Asn Ser His Met Lys Phe Asn
165 170

<210> 284
<211> 46
<212> PRT
<213> Pinus radiata

<400> 284
Met Ala Thr Gly Gly Gly Ala Leu Asp Leu Ala Ser Gly Met Gly Gly
1 5 10 15
Asn Ile Glu Lys Glu Gln Met Leu Thr Ala Val Glu Glu Tyr Glu Lys
20 25 30
Tyr His Met Tyr Tyr Gly Gly Asp Glu Gly Ser Arg Lys Ser
35 40 45

<210> 285
<211> 137
<212> PRT
<213> Eucalyptus grandis

<400> 285
Met Ser Lys Ala Gly Ala Met Asp Leu Ala Thr Gly Leu Gly Gly Lys
1 5 10 15
Met Asp Lys Ser Asp Val Leu Ser Ala Val Asp Lys Tyr Glu Lys Tyr
20 25 30
His Val Cys Tyr Gly Gly Asp Glu Glu Glu Arg Arg Ala Asn Tyr Ser
35 40 45
Asp Met Val Asn Lys Tyr Tyr Asp Leu Ala Thr Ser Phe Tyr Glu Phe
50 55 60
Gly Trp Gly Glu Ser Phe His Phe Ala His Arg Trp Lys Gly Glu Ser
65 70 75 80
Leu Arg Glu Ser Ile Lys Arg His Glu His Phe Leu Ala Leu Gln Leu
85 90 95
Gly Leu Lys Pro Gly His Lys Val Leu Asp Val Gly Cys Gly Ile Gly
100 105 110
Gly Pro Leu Arg Glu Ile Ala Arg Phe Ser Ser Ala Ser Val Thr Gly
115 120 125
Leu Asn Asn Asn Glu Tyr Gln Ile Thr
130 135

<210> 286
<211> 117
<212> PRT
<213> Pinus radiata

<400> 286
Phe Arg Ile Trp Phe Asp Val Pro Val Val Leu Pro Pro Leu Thr Gln
1 5 10 15
Cys Phe Ala Asp Arg Ile Ser Leu Val Tyr Asp Pro His Thr Asp Glu
20 25 30

Tyr Tyr Asn Ala Pro Gly Val Glu Thr Arg Val Pro Tyr Phe Gly Ser
        35   40   45
Thr Glu Gly Met Lys Tyr Leu Asp Pro Cys Phe Lys Tyr Ile Thr Pro
    50   55   60
Tyr Met Ser Ser Leu Val Lys Ser Leu Glu Asp Val Gly Tyr Val Asp
65   70   75   80
Gly Lys Ser Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Pro Gly
                85   90   95
Thr Lys Ser Ser Ser Val Gly Ala Lys Tyr Leu Glu Asn Leu Arg Lys
            100   105   110
Leu Val Glu Glu Ala
        115

<210> 287
<211> 27
<212> PRT
<213> Eucalyptus grandis

<400> 287
Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala Gly Phe Tyr
1   5   10   15
Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser
            20   25

<210> 288
<211> 158
<212> PRT
<213> Pinus radiata

<400> 288
Phe Ala Val Val Gly Pro Leu Gln Leu Thr Ser Tyr Pro Leu Ile Lys
1   5   10   15
Leu Val Gly Ile Arg Thr Gly Leu Pro Leu Pro Ser Leu Trp Glu Ile
            20   25   30
Phe Ala Gln Leu Ala Val Tyr Phe Met Val Glu Asp Tyr Gly Asn Tyr
        35   40   45
Trp Ile His Arg Trp Leu His Cys Lys Trp Gly Tyr Glu Lys Ile His
    50   55   60
His Val His His Glu Phe Thr Ala Pro Met Gly Phe Ala Ala Pro Tyr
65   70   75   80
Ala His Trp Ser Glu Val Leu Ile Leu Gly Ile Pro Thr Phe Val Gly
                85   90   95
Pro Ala Ile Ala Pro Gly His Met Ile Thr Phe Trp Cys Trp Val Val
            100   105   110
Leu Arg Gln Val Glu Ala Ile Glu Thr His Ser Gly Tyr Asp Phe Pro
        115   120   125
Trp Thr Leu Thr Lys Leu Ile Pro Phe Tyr Gly Gly Ala Glu Tyr His
    130   135   140
Asp Tyr His His Tyr Val Gly Gly Gln Ser Gln Ser Asn Phe
145   150   155

<210> 289
<211> 113
<212> PRT
<213> Eucalyptus grandis

<400> 289
Pro Ser Leu Trp Glu Ile Leu Ala Gln Leu Leu Val Tyr Phe Leu Ile
1   5   10   15
Glu Asp Tyr Thr Asn Tyr Trp Leu His Arg Leu Leu His Cys Lys Trp
            20   25   30

Gly Tyr Glu Lys Ile His Ser Val His His Glu Tyr Ser Ala Pro Ile
35 40 45
Gly Phe Ala Ala Pro Tyr Ala His Trp Ala Glu Val Leu Ile Leu Gly
50 55 60
Ile Pro Ser Phe Leu Gly Pro Ala Ile Val Pro Gly His Met Ile Thr
65 70 75 80
Leu Trp Leu Trp Ile Ala Leu Arg Gln Ile Glu Ala Ile Asp Tyr Ser
85 90 95
Gln Arg Val Arg Ile Ala Leu Glu Ser Tyr Glu Val His Ser Ile Leu
100 105 110
Trp

<210> 290
<211> 128
<212> PRT
<213> Eucalyptus grandis

<400> 290
Gly Tyr Gly Ser Met Val Gln Asn Cys Val Lys Ala Arg Ser Leu Leu
1 5 10 15
Ser Lys Leu Gly Ile Glu Val Thr Val Ala Asp Ala Arg Phe Cys Lys
20 25 30
Pro Leu Asp Ile Gly Leu Leu Arg Glu Leu Cys Glu Asn His Ala Phe
35 40 45
Leu Val Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val
50 55 60
Ala Gln Phe Ile Ala Leu Asp Gly Arg Leu Asp Gly Arg Ile Lys Trp
65 70 75 80
Arg Pro Ile Val Leu Pro Asp Ala Tyr Val Glu His Thr Ser Pro Asn
85 90 95
Glu Gln Leu Ser Leu Ala Gly Leu Thr Gly His His Ile Ala Ala Thr
100 105 110
Val Leu Ser Leu Leu Gly Arg Thr Arg Glu Ala Leu Leu Leu Met Cys
115 120 125

<210> 291
<211> 109
<212> PRT
<213> Pinus radiata

<400> 291
Met Ala Val Val Val Ser Ala Pro Gly Lys Val Leu Ile Thr Gly Ala
1 5 10 15
Tyr Leu Ile Leu Glu Lys Pro Asn Pro Gly Leu Val Leu Thr Thr Thr
20 25 30
Ala Arg Phe Tyr Ala Ile Val Lys Pro Leu Arg Thr Ser Thr Asp Ser
35 40 45
Ser Ser Trp Ala Trp Leu Trp Thr Asp Val Lys Leu Thr Ser Pro Gln
50 55 60
Leu Ala Lys Glu Ala Ile Tyr Lys Leu Ser Leu Lys Thr Leu Ser Leu
65 70 75 80
Gln Asn Val Ala Ser Ser Ser Ser Asn Gly Asn Pro Phe Val Glu Gln
85 90 95
Ala Val Gln Phe Ala Val Ala Ala Ala Lys Glu Ala Phe
100 105

<210> 292
<211> 107
<212> PRT
<213> Eucalyptus grandis

<400> 292
Met Ala Gly Glu Trp Ile Leu Thr Leu Thr Ala Gln Thr Pro Thr Asn
1 5 10 15
Ile Ala Val Ile Lys Tyr Trp Gly Lys Arg Asp Glu Ser Leu Ile Leu
20 25 30
Pro Val Asn Asp Ser Ile Ser Val Thr Leu Asp Pro Gly His Leu Cys
35 40 45
Thr Thr Thr Thr Val Ala Val Ser Pro Ala Phe Glu Gln Asp Arg Met
50 55 60
Trp Leu Asn Gly Lys Glu Ile Ser Leu Ser Gly Asp Arg Phe Gln Ser
65 70 75 80
Cys Leu Arg Glu Ile Arg Ala Arg Ala Thr Asp Val Glu Asn Lys Glu
85 90 95
Lys Gly Ile Lys Ile Ser Lys Lys Asp Trp Glu
100 105

<210> 293
<211> 148
<212> PRT
<213> Pinus radiata

<400> 293
Pro Leu Thr Leu Leu Leu Ala Asn Thr Trp Ala Ser Ser Ala Ile Val
1 5 10 15
Ser Arg Arg Val Ser Leu Phe Val Ala Cys Ser Thr Thr Val Val Ser
20 25 30
Arg Ser Phe Ser Lys Ser Cys Ser Gly Ala Ile Pro Arg Lys Pro Lys
35 40 45
Ser Ala His Pro Ala Leu Thr Gly Ser Arg Thr Cys Phe Ser Arg Asn
50 55 60
Pro Ile Val Arg Asn Leu Ile Gly Ser Ala Ser Lys Met Gly Ala Thr
65 70 75 80
Val Glu Asp Thr Thr Met Asp Ala Val Gln Arg Arg Leu Met Phe Glu
85 90 95
Asp Glu Cys Ile Leu Val Asp Glu Glu Asp His Val Ile Gly His Asp
100 105 110
Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ser Glu Asn Leu
115 120 125
Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Thr Lys Tyr Glu Leu
130 135 140
Leu Leu Gln Gln
145

<210> 294
<211> 137
<212> PRT
<213> Eucalyptus grandis

<400> 294
Pro Leu Leu Leu Leu Leu Leu Leu Arg Tyr Pro Ser Pro Leu Pro Pro
1 5 10 15
Arg Pro Ser Leu Ser Leu Cys Arg Ser Thr Ala Met Ala Asp Gly Ala
20 25 30
Asp Ala Gly Met Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu
35 40 45
Cys Ile Leu Val Asp Glu Asn Asp Asn Val Val Gly His Glu Ser Lys
50 55 60
Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ser Leu Asn Leu Leu His
65 70 75 80
Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu

```
                85                      90                      95
Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn
            100                     105                     110
Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Ala Glu
        115                     120                     125
Asn Ala Leu Gly Ala Arg Asn Ala Ala
    130                     135

      <210> 295
      <211> 136
      <212> PRT
      <213> Pinus radiata

      <400> 295
Ala Gly Glu Asn Leu Asp Asn His Val Asp Val Lys Asn Ile Leu Val
1               5                   10                  15
Gln Met Gly Thr Tyr Phe Gln Val Gln Asp Asp Tyr Leu Asp Cys Phe
            20                  25                  30
Gly Asp Pro Glu Val Ile Gly Lys Ile Gly Thr Asp Ile Glu Asp Phe
        35                  40                  45
Lys Cys Ser Trp Leu Val Val Gln Ala Leu Glu Arg Ala Asn Glu Ser
    50                  55                  60
Gln Leu Gln Arg Leu Tyr Ala Asn Tyr Gly Lys Thr Asp Pro Ser Cys
65                  70                  75                  80
Val Ala Glu Val Lys Ala Val Tyr Arg Asp Leu Gly Ile Gln Asp Val
                85                  90                  95
Phe Phe Glu Tyr Glu Arg Thr Ser Tyr Lys Glu Leu Ile Ser Ser Ile
            100                 105                 110
Glu Ala Gln Glu Asn Glu Ser Leu Gln Leu Val Leu Lys Ser Phe Leu
        115                 120                 125
Gly Lys Ile Tyr Lys Arg Gln Lys
    130                 135

      <210> 296
      <211> 83
      <212> PRT
      <213> Pinus radiata

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Pro Lys Lys Ile Gly Ile Ala Glu Glu Val Phe Val Val Asp Leu Lys
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Ile Phe Pro Lys Pro Ser Lys Met
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PCT

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Published

With international search report.
Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(88) Date of publication of the international search report: 3 August 2000 (03.08.00)

(54) Title: MATERIALS AND METHODS FOR THE MODIFICATION OF ISOPRENOID CONTENT, COMPOSITION AND METABOLISM

(57) Abstract

Novel isolated polynucleotides associated with plant isoprenoid biosynthetic pathways are provided, together with genetic constructs comprising such sequences. Methods for the modulation of the content, structure and metabolism of polypeptides involved in an isoprenoid biosynthetic pathway in target organisms are also disclosed, the methods comprising incorporating one or more of the polynucleotides or genetic constructs of the present invention into the genome of a target organism. Modulation of the content, structure and metabolism of such polypeptides produces modifications in the content, structure and metabolism of isoprenoids in the target organism.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. 7: C12N 5/10, 9/00, 15/29, 15/63

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Databases below.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Details in Supplemental Box V.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank accession AJ011840 submitted 7 October 1998 by Clastre M.	1-29
X	GenBank accession AF019383 submitted 14 August 1997 by Lange BM et al.	1-29
X	GenBank accession Y15782 submitted 4 December 1997 by Camara B.	1-29
X	GenBank accession Y14333 submitted 28 July 1997 by Camara B.	1-29
X	GenBank accession AB003156 submitted 2 May 1997 by Suzuki H.	1-29

[X] Further documents are listed in the continuation of Box C [ ] See patent family annex

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
5 June 2000	09 JUNE 2000

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank accession D78130 submitted 12 October 1995 by Sakakibara J et al.	1-29
X	GenBank accession AF061285 submitted 24 April 1998 by Back K et al.	1-29
X	GenBank accession U87908 submitted 31 January 1997 by Bohlmann J et al.	1-29
X	GenBank accession U87909 submitted 31 January 1997 by Bohlmann J et al.	1-29
X	GenBank accession AF006193 submitted 30 May 1997 by Bohlmann J et al.	1-29
X	GenBank accession U92266 submitted 5 March 1997 by Steele CL et al.	1-29
X	GenBank accession AF006195 submitted 30 May 1997 by Bohlmann J et al.	1-29
X	GenBank accession U60542 submitted 12 June 1996 by Kollipara KP et al.	1-29
X	GenBank accession L10390 submitted 22 September 1993 by Burnett RJ et al.	1-29
X	GenBank accession X54657 submitted 29 August 1990 by Chye ML.	1-29
X	GenBank accession U72146 submitted 21 September 1996 by Maldonado-Mendoza IE and Nessler CL.	1-29
X	GenBank accession X68652 submitted 7 October 1992 by Bach TJ.	1-29
X	GenBank accession X68651 submitted 7 October 1992 by Bach TJ.	1-29
X	GenBank accession X54659 submitted 29 August 1990 by Chye ML et al.	1-29
X	GenBank accession X15032 submitted 18 April 1989 by Caelles C.	1-29
X	GenBank accession M96068 submitted 27 April 1993 by Maldenado-Mendoza IE et al.	1-29
X	GenBank accession X96429 submitted 5 March 1996 by Chen XY et al.	1-29
X	GenBank accession U27535 submitted 23 May 1995 by Chen XY et al.	1-29
X	GenBank accession AB009029 submitted 20 November 1997 by Kushiro T.	1-29
X	GenBank accession AB009031 submitted 20 November 1997 by Kushiro T.	1-29
X	GenBank accession D89619 submitted 28 November 1996 by Shibuya M.	1-29
X	GenBank accession U02555 submitted 15 October 1993 by Matsuda SP.	1-29
X	GenBank accession U74319 submitted 15 October 1996 by Bak S et al.	1-29
X	GenBank accession Y09291 submitted 6 November 1996 by Weerck-Reichhart.	1-29

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank accession AB014057 submitted 15 May 1998 by Kushiro T et al.	1-29
X	GenBank accession AB00930 submitted 20 November 1997 by Kushiro T.	1-29
X	GenBank accession Z83833 submitted 10 January 1997 by Warnecke D.	1-29
X	GenBank accession Z83832 submitted 10 January 1997 by Warnecke D.	1-29
X	GenBank accession U81312 submitted 7 December 1996 by Benveniste P.	1-29
X	GenBank accession U81313 submitted 7 December 1996 by Benveniste P.	1-29
X	GenBank accession AF045570 submitted 30 January 1998 by Tong Y and Nes WD.	1-29
X	GenBank accession U79669 submitted 25 November 1996 by Grebenok RJ et al.	1-29
X	GenBank accession U43683 submitted 20 December 1995 by Clouse JA.	1-29
X	GenBank accession U60205 submitted 6 June 1996 by Kaplan J and Li L.	1-29
X	GenBank accession U93162 submitted 11 March 1997 by Herrmann K.	1-29
X	GenBank accession D50559 submitted 15 May 1995 by Uwebe K.	1-29
X	GenBank accession U27099 submitted 12 May 1995 by Mandel MA et al.	1-29
X	GenBank accession Y14325 submitted 24 July 1997 by Cordier H.	1-29
X	GenBank accession U53706 submitted 6 April 1996 by Jeng CJ and Schweitzer ES.	1-29
X	GenBank accession U49260 submitted 15 February 1996 by Toth MJ et al.	1-29
X	GenBank accession Y17593 submitted 17 June 1998 by Cordier H.	1-29
X	GenBank accession Y09292 submitted 6 November 1996 by Werck-Reichhart D.	1-29
X	GenBank accession U50201 submitted 28 February 1996 by Poulton JE and Jurk S.	1-29
X	GenBank accession AF072736 submitted 16 June 1998 by Dharmawardhana D et al.	1-29
X	GenBank accession X56734 submitted 19 November 1990 by Hughes MA.	1-29
X	GenBank accession D83177 submitted 19 January 1996 by Inoue K.	1-29
X	GenBank accession U39228 submitted 23 October 1995 by Wiersma PA.	1-29
X	GenBank accession U26025 submitted 2 May 1995 by Zheng L and Poulton JE.	1-29

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

C (Continuation). **DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank accession AB017026 submitted 20 August 1998 by Snider J et al.	1-29
X	GenPept accession CAA03409 submitted 21 August 1996 by Chenivesse X et al.	1-29
X	GenPept accession CAA76803 submitted 17 June 1998 by Cordier H.	1-29
X	AU, A 24637/99 (WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION) 21 January 1999 A01H 5/00, C07K 14/415, C12N 1/00, 5/04, 5/06, 9/00, 15/29, 15/52, 15/74, 15/79, 15/82, 15/84. See entire document.	1-29

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

Box I — Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :

   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos : **1, part (11); 1, part (12); 2; 26, part (7); 26, part (8).**

   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

   These claims refer to polynucleotide or polypeptide sequences comprising 40, 20 or 10 contiguous residues of sequences provided in SEQ. ID. NOs: 1-53, 78-286, 288-304. The scope of the claims encompasses many sequence fragments and it is not economically viable to search all possible combinations.

3. ☐ Claims Nos :

   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II — Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Continued in Supplemental Box

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No. PCT/NZ99/00219

Supplemental Box I
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

The International Searching Authority has found that there are 37 separate inventions, wherein a single enzyme or protein type provides the special technical feature.

1. Nucleic and amino acid sequences SEQ. ID. NOs: 1, 252 encoding acetylcholinesterase precursor, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

2. Nucleic and amino acid sequences SEQ. ID. NOs: 2, 253 encoding deoxyxylulosephosphate synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

3. Nucleic and amino acid sequences SEQ. ID. NOs: 3, 4, 44, 254, 255, 295 encoding geranyltranstransferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

4. Nucleic and amino acid sequences SEQ. ID. NOs: 5, 6, 256, 266 encoding farensyltranstransferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

5. Nucleic and amino acid sequences SEQ. ID. NOs: 7, 154, 258, 241 encoding squalene synthetase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

6. Nucleic and amino acid sequences SEQ. ID. NOs: 8-10, 155-157, 259-261, 242-244 encoding squalene monooxygenase. DNA probes or primers therefrom, transgenic cells and constructs containing the sequences. and methods of modulating biosynthesis of isoprenoid content and metabolism.

7. Nucleic and amino acid sequences SEQ. ID. NOs: 11, 82, 83, 262, 169, 170 encoding geranylgeranyl-diphosphate geranylgeranyltransferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

8. Nucleic and amino acid sequences SEQ. ID. NOs: 12, 263 encoding trichodiene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

9. Nucleic and amino acid sequences SEQ. ID. NOs: 13, 25-27, 84-88, 95, 115-118, 264, 276-278, 171-175, 182, 202-205 encoding pinene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

10. Nucleic and amino acid sequences SEQ. ID. NOs: 14, 89, 90, 265, 176, 177 encoding abietadine synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

Continued in Supplemental Box II

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

Supplemental Box II
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Supplemental Box I

11. Nucleic and amino acid sequences SEQ. ID. NOs 15. 32. 91-94. 96-98, 131-135. 266. 283. 178-181. 183-185, 218-222 encoding hydroxymethylglutaryl-CoA reductase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

12. Nucleic and amino acid sequences SEQ. ID. NOs: 16-18, 99-102, 267-269, 186-189 encoding myrcene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

13. Nucleic and amino acid sequences SEQ. ID. NOs: 19, 20, 26, 27, 103, 107, 108, 277, 278, 270, 271, 190, 194, 195 encoding limonene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

14. Nucleic and amino acid sequences SEQ. ID. NOs: 21-23, 109-111, 272-274, 196-198 encoding cadinene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

15. Nucleic and amino acid sequences SEQ. ID. NOs: 24, 114, 275, 201 encoding bisabolene synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

16. Nucleic and amino acid sequences SEQ. ID. NOs: 28, 119-122, 279, 206-209 encoding cycloartenol synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

17. Nucleic and amino acid sequences SEQ. ID. NOs: 29, 124-126, 280, 211-213 encoding obtusifoliol demethylase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences. and methods of modulating biosynthesis of isoprenoid content and metabolism.

18. Nucleic and amino acid sequences SEQ. ID. NOs: 30, 281 encoding lupeol synthase, DNA probes or primers therefrom. transgenic cells and constructs containing the sequences. and methods of modulating biosynthesis of isoprenoid content and metabolism.

19. Nucleic and amino acid sequences SEQ. ID. NOs: 31, 158, 159, 282, 245, 246 encoding udp-glucose:sterol glucosyltransferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

20. Nucleic and amino acid sequences SEQ. ID. NOs: 33, 34, 160-162, 284, 285, 247-249 encoding sterolmethyltransferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

Continued in Supplemental Box III

Supplemental Box III
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Supplemental Box II

21. Nucleic and amino acid sequences SEQ. ID. NOs: 35, 136, 286, 223 encoding lecithin:cholesterol acyl transferase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

22. Nucleic and amino acid sequences SEQ. ID. NOs: 36, 137, 287, 224 encoding sterol delta-7 reductase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

23. Nucleic and amino acid sequences SEQ. ID. NOs: 37, 38, 138-140, 288, 289, 225-227 encoding methyl sterol oxidase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

24. Nucleic and amino acid sequences SEQ. ID. NOs: 39, 290 encoding deoxyxylulosephosphate synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

25. Nucleic and amino acid sequences SEQ. ID. NOs: 40, 291 encoding phosphomevalonate kinase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

26. Nucleic and amino acid sequences SEQ. ID. NOs: 41, 50, 141, 142, 146, 292, 301, 228, 229, 233 encoding diphosphomevalonate decarboxylase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

27. Nucleic and amino acid sequences SEQ. ID. NOs: 42, 43, 143, 293, 294, 230 encoding isopentenyl-diphosphate delta-isomerase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

28. Nucleic and amino acid sequences SEQ. ID. NOs: 45, 296 encoding estradiol dehydrogenase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

29. Nucleic and amino acid sequences SEQ. ID. NOs: 46-49, 144, 145, 297-300, 231-232 encoding furostanol glucosidase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

30. Nucleic and amino acid sequences SEQ. ID. NOs: 51, 52, 147-153, 302, 303, 234-240 encoding oxysterol-binding protein, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

Continued in Supplemental Box IV

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ99/00219

Supplemental Box IV
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Supplemental Box III

31. Nucleic and amino acid sequences SEQ. ID. NOs: 53, 304 encoding sterol carrier protein. DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

32. Nucleic and amino acid sequences SEQ. ID. NOs: 78, 79, 127-130, 165, 166, 214-217 encoding sterol 14-demethylase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

33. Nucleic and amino acid sequences SEQ. ID. NOs: 82, 83, 169, 170 encoding geranylgeranyl diphosphate, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

34. Nucleic and amino acid sequences SEQ. ID. NOs: 104-106, 164, 191-193, 251 encoding CXPS/transketolase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

35. Nucleic and amino acid sequences SEQ. ID. NOs: 112, 113, 199, 200 encoding sabinene synthase. DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

36. Nucleic and amino acid sequences SEQ. ID. NOs: 123, 210 encoding beta-amyrin synthase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

37. Nucleic and amino acid sequences SEQ. ID. NOs: 163, 250 encoding sterol desaturase, DNA probes or primers therefrom, transgenic cells and constructs containing the sequences, and methods of modulating biosynthesis of isoprenoid content and metabolism.

The above inventions have been allocated into the following groups for searching purposes:

A: Inventions 1 to 6.
B: Inventions 7 to 10.
C: Inventions 11 and 12.
D: Inventions 13 to 15.
E: Inventions 16 to 20.
F: Inventions 21 to 26.
G: Inventions 27 to 30.
H: Inventions 31 to 37.

Supplemental Box V
(To be used when the space in any of Boxes I to VIII is not sufficient)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used):

GenBank, EMBL, PDB Nucleic Acids, SWISS-PROT, GenPept, PIR, TREMBL - SEQ. ID. NOs: 1-53, 78-286, 288-304

WPIDS: Keywords used - acetylcholinesterase precursor, deoxyxylulosephosphate synthase, dxps, geranyltranstransferase, farnesyl diphosphate synthase, farnesyltranstransferase, farnesyl diphosphate farnesyltransferase, presqualene diphosphate, squalene synthetase, squalene monooxygenase, squalene epoxidase, geranylgeranyl diphosphate geranylgeranyltransferase, prephytoene diphosphate synthase, trichodiene synthase, pinene synthase, abietadine synthase, hydroxymethylglutaryl coa reductase, myrcene synthase, limonene synthase, cadinene synthase, bisabolene synthase, cycloartenol synthase, epoxysqualene cycloarteno cyclase, obtusifoliol demethylase, lupeol synthase, udp glucose sterolglucosyl transferase, sterol glucosyltransferase, sterolmethyltransferase, lecithin cholesterol acyl transferase, phospholipid cholesterol acyltransferase, sterol delta 7 reductase, methyl sterol oxidase, deoxyxylulosephosphate synthase, dxps, diphosphomevalonate decarboxylase, phosphomevalonate kinase, isopentenyl diphosphate delta isomerase, estradioldehydrogenase, furostanol glucosidase, oxysterol binding protein, sterol carrier protein, sterol 14 demethylase, sesquiterpene cyclase, trichodiene synthase, cxps transketolase, sabinene synthase, beta amyrin synthase, sterol desaturase, pinus radiata, p radiata, pine, or pinus, eucalyptus grandis, e grandis, eucalyptus, isoprenylation, isoprenoid

INTERNATIONAL SEARCH REPORT

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
AU	24637/99	WO	9937139

END OF ANNEX